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Result
No.
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Maximum
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-MODEL-frame+ p2n.model -DEV=xlh
-Q-/Ggn2_1/USPTO_Spool_h/US10627571/runat_27072005_154720_27503/app_query.fasta_1.327
-DB=GenEmb1 -QFMT=fastap -SUFFIX==ge -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US10627571_@CGN 1 1 3731 @runat 27072005 154720 27503 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
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Perfect score:
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                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BG
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seq length: 2000000000
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Ygapop 10.0 , y
Fgapop 6.0 , F
Delop 6.0 , D
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Copyright (c) 1993 - 2005 Compugen Ltd
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REFERENCE
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SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (05-JUN-1998) Biochemistry, Academic Media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens TNF-induced AF070671
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1892)
Horrevoets, A.J.G., Fontijn, R.D. and Pannekoek, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1892)
Horrevoets, A.J., Fontijn, R.D., van Zonneveld, A.J., de Vries, C.J.,
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/product="TNF-induced protein GG2-1"
/protein id="AACB3229.1"
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VVSFHQVDYTPRNVLSRILNECREMLHQIIQHHLTAKSHGRVNNVFDHFSDCEFLAA
LYNPFGNFKPHLQKLCDGINKMLDEENI"
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/cell_type="endothelial"
/tlssue_type="umbilical vein"
/8. .664
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AX024161
AX898564
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1921)

1 (bases 1 to 1921)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11723 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/11723
PD 09-JUL-2000
PF 28-JUL-2000 JP 2000280990
PF 28-JUL-2000 JP 2000280900
PF 28-JUL-2000 JP 2000280900
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JP 2002191363-A/11723.
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JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
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AAAATGTTGGATGAAGAGAACATA 703
              LysMetLeuAspGluGluAsnIle 188
                                                                      LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
                                                                                                              TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
                                                                                                                              SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                                                    CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
                                                                                                                                                                                   LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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                                                       TTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAAC
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679 180 619 140

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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 12751 07-FEB-2001;
Research Association for Biotechnology (JP)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK001931
AK001931.1 GI:7023502
oligo capping; fis (full insert sequence)
Homo sapiens (human)
                                                                                                                                                                                                            Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisaravi, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sasaki,N.
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Nat. Genet. 36 (1), 40-45 (2004)
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                                                                                                                                                                                  etc.) and Department University of Tokyo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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sapiens cDNA FLJ11069 fis, clone PLACE1004930,
omo sapiens MDC-3.13 isoform 2 mRNA.
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                                                                                                                                                                                           Homo sapiens full open reading frame cDNA clone RZPDO834H127D for gene TNFAIP8, tumor necrosis factor, alpha-induced protein 8; complete cds, incl. stopcodon.
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Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 573) 
Ebert, L., Schick, M., Neubert, P., Schatten, R., Cloning of human full open reading frames in Gentry vector (pDONR201)
                                                                                                                                             CR457137.1 GI:48146390 Full ORF shuttle clone,
                                                                                                            Homo sapiens (human)
                                                                                                                                                                                 complete cds, CR457137
                                                                                                                                                                                                                                                                                                                                           LysMetLeuAspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="placenta"
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/note="cloning vector: pME18SFL3"
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954.00
99.47%
99.47%
99.17%
                                                                           Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                             Gateway (TM), complete cds
                                                                                                                                                                                                                                                                                                                             703
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                      in Gateway(TM) system
                                                                           Hominidae;
                                                                           Euteleostomi; Homo.
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319 60 259

199

80

160

559 140 499 120

619

679

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                          Match:
                   67
                                   21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide.
The stop codon has been set to TAA followed by
TTAACCCAGCTTTCTT. .att. Compared to the reference sequence NM_014350
we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contact RZPD (customer service@rzpd.de) for further informati This CDS clone is a part of a collection of human full length expression clones generated by RZPD.

This CDS has been cloned incl. stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase (TM) reaction. Additional sequence has been added in front of the codon: att. .AAAAAA GCA GGC (ATG).

The last base of the last coding triplett has been changed to which might lead to an amino acid change at the C terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Germany
RZPD; RZPDO834H127D, ORFNO 1910
RZPD; RZPDO834H127D RZPDLIB;
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDO834H127D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (03-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Submitted (03-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available from RZPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +49 30 32639 100 Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.rzpd.de/products/orfclones/
Contact: Inge Arlart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
                                                                                                          GGTAAAATGGTGTCCAAATCCATCGCCACCATCATAGACGACACAAGTAGTGAGGTG
                                                                                   GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG
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                                                                                                                                                                                                                                                                                                                                     /gene="TNFAIP8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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Schick,M., Neubert,P., Schatten,R., Henze,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH1OB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="TNFAIP8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="RZPDo834H127D"
                                                                                                                                                                                                     6.04e-76
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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186
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Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer for BD156785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD156785.1 GI:27862543 JP 2002191363-A/11628.
                                                                                                                                                                                                                                                                                                                                                                                                                HELIX RESEARCH INSTITUTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD156785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                            SAITO
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                                                                                                                                                                                                                                                                                                                                                                              JP 2002191363-A/11628
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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 1.89e-75
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181 LysMetLeuAspGluGluAsnIle 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
                                                                                                                                   PC C12P21/U2/LILE
Primer for synthesizing full-I
Location/Qualifiers
(71). (6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J. Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNa and use thereof Patent: JP 2002191363-A 11628 09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1729)
                                                                                                                                                                                                                                                                                        C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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                                                                                                                                                                                                                               C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
                                                                                                                                                                                                                                                                                                                                              JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000 JF 2000280990
TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
                                                                                                                 Location/Qualifiers
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full-length
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Length:

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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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AX877673
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                                                               Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Saito,K., Yamamoto,J., Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 12578 07-FEB-2001; Research Association for Biotechnology (JP)
Location/Qualifiers
1. 1729
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Sequence 12578 from Pate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Ota,T., Suzuki,Y., Nishikawa,T., Ot
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                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                AK001850
AK001850.1 GI:7023373
oligo capping; fis (full
Homo sapiens (human)
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US-10-627-571-2 (1-188) x AX877673
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                       LysMetLeuAspGluGluAsnIle
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Otsuki,T., (

Sugiyama, T., Kimura, K.,

Makita, H.,

'n

Hominidae;

Euteleostomi;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1522-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
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Isogai,T. and Otsuki,T.
Direct Submission
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98.75%
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Matches:
Conservative:
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                                                                                                                                                                      Mismatches:
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RESULT 9
BC005352
LOCUS
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                 HITLE
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                     RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., Kodrigues, S.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LysMetLeuAspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641 AAAATGTTGGATGAAGAGAACATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 ATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1814)
1 (consecutive formula 
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1814 bp mRNA linear PRI 24 Homo sapiens tumor necrosis factor, alpha-induced protein (CDNA clone MGC:12451 IMAGE:3997650), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGGCAGAGAAG
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REFERENCE
AUTHORS
TITLE
JOURNAL
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COMMENT
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                                                                                                                                               Match:
    174
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                     MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG
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DTSSEVLDELYRVTREYTQNKKBAEKIIKNLIKTVIKLAILYRNNQFNQDELALMEKF
KKKVHQLAMTVVSFHQVDYTEDRNVLSRLLNEGCEMLHQIIQRHLTAKSHGRVNNVFD
HFSDCEFLAALYNFFGNFKPHLQKLCDGINKMLDEENI"
                                                                                                                                                                                                                                                                                                      (DUF758). Family of eukaryotic function, which are induced by /db_xref="CDD:pfam05527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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/tissue_type="Bladder, carcinoma"
/clone_lib="NIH_MGC_53"
/lab_host="DH10B"
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/db_xref="GI:13529164"
                                                                                                                                                                                                                                                                                                                                                                 note="DUF758; Region: Domain of unknown
                                                                                                                                                                                                                                                                                                                                                                                      /gene="TNFAIP8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="LocusID:25816"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TNFAIP8"
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144. .740
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Submitted (13-OCT-1998) Max Planck Institute for Molecular Senetics, Inneserrasse 73, Berlin 14195, Germany
Location/Qualifiers
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Nietfeld, W. and Meyerhans, A.F. Identification of cellular fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens MDC-3.13 isoform AF099935 AF099935.1 GI:3860092
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Nietfeld, W. and Meyerhans, A.F.
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/mol_type="mRNA"
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Sequence 120
CQ726075
CQ726075.1
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                                                          Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and oth
                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  Patent: WO 02068579-A 12009 06-SEP-2002; PE Corporation (NY) (US)
                                                 thereof
                                                                                                                                                                 Homo sapiens (human)
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    Location/Qualifiers
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HFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI "
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2003)
Nietfeld,W. and Meyerhans,A.F.
Identification of cellular factors involved in the dof dendritic cells
Unpublished
2 (bases 1 to 2003)
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Homo sapiens MDC-3.13 isoform
AF099936
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                                         LysMetLeuAspGluGluAsnIle 188
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                                gene
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNI at: http://image.lln1.gov Series: IRAL Plate: 16 Row: b Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657123.
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
McKernan, K.J., Malek, J.A., Gounaratne, P.H., Richards, S.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Bouffard, G.G., Blakesley, R. W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens tumor necrosis factor, alpha-induced protein 8, mRNA
(cDNA clone MGC:12346 IMAGE:3930240), complete cds.
BC007014
                                                                         cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 943 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (30-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, R. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.2.
STS Content:
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On Apr 27, 2001 this sequence version replaced gi:7712094
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Quality: Phrap Quality >
Estimated Total Number o
STS Content:
SHGC-7119 G14211.
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Submitted (21-SEP-2001) DOE Joint Genome Institute, 2800 M:
Drive, Walnut Creek, CA 94598, USA
On Sep 21, 2001 this sequence version replaced gi:15383783
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Direct Submission

Submitted (31-AUG-2001) DOE Joint Genome Institute,
Submitted Walnut Creek, CA 94598, USA
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Submitted (24-MAR-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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DOE Joint Genome Institute and Stanford Human Genome Cer
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DOE Joint Genome Institute and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 158057)
Sulston, J.E. and Wilson, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                         Direct Submission
Submitted (11-JAN-2003) Genome
University School of Medicine,
MO 63108, USA
4 (bases 1 to 158057)
Wilson, R.
Direct Submission
Submitted (30-MAY-2003)
                                                                                                                                                                   3 (bases 1 to 158057)
Waterston, R.H.
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Tomlinson,C. and Bielicki,L.
The sequence of Homo sapiens
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >> 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence as compressions and repeats; all resions were covered by sequence form more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selection:
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Clone CTD-2293E22 i
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                   /rpt_family="L1" 5767. .6328
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mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="2"
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/rpt_family="MaLR"
8621. .8849
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9113. .9415
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|5273. .15541
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7503. .7872
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG
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                                            LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
                                                                                                    SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                                           LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                   ATGACCGTGGTCAGTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
                                                                                                                                                                                                                                                                                                                                                                           CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                          LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
LysMetLeuAspGluGluAsnIle 188
                                                                                                                                            CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
                                                                                                                                                                                                                    MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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                          TTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAAC
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ACCESSION
VERSION
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BD135356
LOCUS
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Percent Similarity:
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HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002508167-A/107
PN JP 2002508167-A/107
PN JP 2002508167-A/107
PN JP 2002508167-A/107
PR 18-DEC-1997 US 60/068 005,18-DEC-1997 US 60/068 007 PR
18-DEC-1997 US 60/068 005,18-DEC-1997 US 60/068 054 PR
18-DEC-1997 US 60/068 064,18-DEC-1997 US 60/068 053 PR
18-DEC-1997 US 60/068 169,19-DEC-1997 US 60/068 054 PR
19-DEC-1997 US 60/068 367,19-DEC-1997 US 60/068 369 PR
19-DEC-1997 US 60/068 369 PR
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1 (bases 1 to 1943)

Moore, P.A., Ruben, S.M., Carter, K.C., Shi, Y., Rosen, C.A.,

Soppet, D.R., Caou, H., Wei, Y.F., Florence, K., Duan, R.D.,

Florence, C., Greene, J.M., Feng, P., Ferrie, A.M., Yu, G.L., Janat, F.
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JP 2002508167-A/107.
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110 human secretory proteins
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2C A61P25/02,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,C12N15/00,A61K37/02,
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                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Homo sapiens (human)'.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
          Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Yamada,T., Kawai,Y., Kodaira,H., Kondo,H., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Kateuta,N., Sato,K., Kikkawa,E., Cujimori,K., Tanai,H., Kimata,M., Watanabe,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanchori,K., Takahashi-Pujii,A., Hara,H., Tansase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Sasaki,N., Actsuka,S., Yoshikawa,Y., Musashino,K., Yuki,H., Oshima,A., Sasaki,N., Sano,S., Moriya,S., Moniyama,H., Satoh,N., Takami,S., Torashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Shudiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Matanabe,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Takemoto, M., Kawakami, B.,
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                                                                                                                                                                                                                                                                                                                                      719 GTGGCCÁCÁGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG
                                                                                                  41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                                                                                        21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 40
61 LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamateari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers
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Isogai, T. and Yamamoto, J.
Direct Submission
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/clone_lib="SPLEN2"
/note="cloning vector: pME18SFL3"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SPLEN2027157"
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RISSTRAUSBERG, R.L., Feingold, E.A., Grouse, L.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diacchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                            Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1952736 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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LysīleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln 80
                                                                                                      LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                                                       GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
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                                                                                                                                                                            GGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCAGGTG
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                                                                      CTAGATGAGCTGTACAGGGTGACCAAGGAGTACACCCAGAACAAGAAGGAGGCGGAGAGG
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/clone="MGC:11714 IMAGE:3965693"
/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAH09090.1"
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KKKVHQLAMTVVSFHQVEYTEDRNVLSRLLNECRELLHEIIQRHLTAKSHGRVNNVFD
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/note="synonyms: Nded, Gg2-1, Ssc-2"
/db_xref="LocusID:106869"
/db_xref="MGI:2147191"
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/mol_type="mRNA"
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/product="TNF-induced
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                                                                                                                                                                                                                                                                                                                                                                                     Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farroira, P., Fitchlugh, W., Gage, D., Galagan, J., Gardyna, S., Gilnde, S., Gord, S., Goyette, M., Gasham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lundblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Ehback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Reetta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ve, W.J., Young, G., Submitted (13.MAY-2002) Whitehead Tretitre, M.T. Gotter, For Gotter, J., Submitted (13.MAY-2002) Whitehead Tretitre, M.T. Gotter, For Gotter, M.T., Submitted (13.MAY-2002) Whitehead Tretitre, M.T., Mercell, M.T., Submitted (13.MAY-2002) Whitehead Tretitre, M.T., Mercell, M.T., Submitted (13.MAY-2002) Whitehead Tretitre, M.T., Mercell, M.T., Mercell,
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                    Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 184327)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Bartien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corm, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farce, S., Ferreira, P., Fitzderald, M., Gage, D., Gage, D., Chang, M., Gage, D., Chang, M., Gooke, P., Cook, A., Cooke, P., Gage, D., Gage, D., Chang, C., Fatzderald, M., Gage, D., Gage, D., Chang, C., Cha
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 18, clone RP24-200D2
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Balloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chaegel, Y., Collymore, A., Cooke, P., Coorum, B., Choegel, Y., Collymore, A., Cooke, P., Coorum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farzo, S., Ferreira, P., FitzGerald, M., Gage, D., Erickson, J., Farzo, S., Graham, L., Grand-Pierre, N., Hafez, N., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Jones, C., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, H., Venkataraman, V. S., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Submitted (No. Aller, 2004) Whitehead Institute/MT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 5, 2004 this sequence version replaced gi:49035085. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                      Center project name: L21053
Center clone name: 200_D_2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
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3. .21837
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                             family="B1_MM"
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                    AUTHORS
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                                                        AC095257.5 GI:24818022

HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus (Sormay rat)

Rattus norvegicus (Sormay rat)

Rattus norvegicus (Sormay rat)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaila; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                            Rattus norvegicus clone CH230-10A12,
1 (bases 1 to 237561)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
                                              Rattus.
                                                                                                                                                                                                                                                                                                                                                 SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
                                                                                                                                                                                                                                                                                                                                                                                                           GTCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCCTCCACAGGAACAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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                                                                                                                                                                                                                                                    LysMetLeuAspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                                            LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGG
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                                                                                                                                                                                                                                    AAAATGTTAGATGAAGAGAACATA 145416
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/rpt family="rx7"
complement (23912. .24049)
/rpt family="B1_MM"
complement (24017. .24236)
/rpt_family="MTC"
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N, WORKING DRAFT SEQUENCE.
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144912 20

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145212 120 145152

145332

145272

Adams, C., Alder, J

HTG 09-NOV-2002

repeat_region

repeat_region

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AL Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:23264563.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Genome Sequencing Consortium.
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                    21 GlyLysMetValSerIysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 40
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JOURNAL REFERENCE AUTHORS TITLE

TITLE

JOURNAL

REFERENCE

JOURNAL AUTHORS

COMMENT

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                   US-10-627-571-2 (1-188) x AC095257 (1-237561)
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95045 GTGGCTACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTG
               table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the accession number will be preserved.

1 237561: contig of 237561 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: CH230-10A12

Assembly program: Phrap; version 0.990329

Assembly program: Phrap; version 0.990329

Consensus quality: 229749 bases at least Q40

Consensus quality: 231209 bases at least Q30

Consensus quality: 232003 bases at least Q20

Estimated insert size: 232575; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
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complement(232422.
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clone_end:T7"
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clone_end:T7
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clone_end:Sp6"
coc__crec
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clone_end:Sp6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                         note="wgs_end_extension
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94.15%
95.43%
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918.00
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RESULT 22
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BD149395
BD149395.1 GI:27855153
JP 2002191363-A/4238.
Homo sapiens (human)
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OS HOMO SADIENS (human)
PN JP 2002191363-A/4238
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAXAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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PC C12P21/02,C12Q1/68//CLLELL,
Primer for synthesizing full-length (
Primer for synthesizing full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 816)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 4238 09-JUL-2002;

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
N 2002191363-A/4238
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                                                                                          /organism='Homo
  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 4238 from Patent EP1074617.
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
                                              1. .816
                                                                 Location/Qualifiers
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                                                         TITLE
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ORFI.

Gallus gallus (chicken)

Gallus gallus (chicken)

Gallus gallus (chicken)

Archosauria; Aves; Neognathae; Charchosauria; Charchosauria; Charchosauria; Charchosauria; Charcho
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        ratuwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M., Placihy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M. Full-length cDNAs from bursal lymphocytes to facilitate gene function analysis
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum,
Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
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                    CTGTTGAATGACTGTAGAGAGCTGCTTCATCAGATCATTCAGCGTCACCTAACTGCGAAA
                                        LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                              AAGACGGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACAGGAATTTCTTGTCCAAA
                                                                                                              MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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YRVTKEYTQNKKEAEKIIKNLIKIVLKLAILYRNNQFNQDEIALMEKFKKKVHQLAKT
VVSFHQVDYTFDRNFLSKLLNDCRELLHQIIQRHLTAKSHGRVNNVFDHFSDCEFLAA
LYNPFGPYKLHLQKLCDGVNRMLDEGNI"
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/locus_tag="RCJMB04_29h8"
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/product="hypothetical protein"
/protein_id="CA832565.1"
/protein_id="CS3136472"
/db_xref="GI:53136472"
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/tissue_type="bursa"
/clone_lib="riken1"
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                                                                                                                                                                              Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.
                              3 (bases 1 to 1766)
Isogai, T. and Yamamoto, J.
Direct Submission
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
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                              nLysMetLeuAspGluGluAsnIle 188
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYMU2004688"
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/clone_lib="THYMU2"
/note="cloning_vector
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This sequence is from a Xenopus Gene Collection (XGC) library, a library constructed by Aaron M. Zorn. cDNA was prepared from extracted from eggs. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end. Vector: pCS107; Site 1: EcoRI; Site 2: NotI Host: Escherichia coli XL1-blue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Voigt, J. and Zorn, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR760636.1 GI:51966545
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                                                                                                                           CAGTTTAATGAGGAAGAGATTGCACTCATGGAGAAGTTCAAGAGAAAGGTCCATCAGCTG
                                                                                                                                                                                                                                                                                                                            AAAGTTATAAAGAACCTCATCAAAACCGTGATCAAGCTGGCAGTCCTGTACAGGAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValLeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGlu
                            AAATTGTTAAATGAGTGCCGGGAGCTGCTCCATCAGGTCATACAGCGCCATCTCACGGCA
                                                      ArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAla 139
                                                                                                                                                                                                                                                                GlnPheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeu
                                                                                                                                                                                                                                                                                                                                                         LysLysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAAGATGGCCTCATCAAAGTACATAGCAACATCCCTTATTGACGATACAAGCGGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus tropicalis"
/mol type="mRNA"
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/clone_lib="XGC-egg"
/dev_stage="egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4e-66
844.50
96.30%
85.19%
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Matches:
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PUBMED
REFERENCE
AUTHORS
TITLE
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COMMENT
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BC072904
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schnutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                              NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                        Direct Submission

Submitted (07-JUN-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein,S.L., Strausberg,R.L., Wagner,L.,
and Richardson,P.
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1 (bases 1 to 1193)

Klein c r
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Xenopus laevis MGC80354 protein, mRNA (cDNA clone MGC:80354
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                     Klein, S. and Gerhard, D.S.
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12454917
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                                                 info@bcgsc.bc.ca
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Query Match:
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy L: Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mor: Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schmerch, Ursula Skalska, Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                   AlaMetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSer 119
                                                                                                           GlnPheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeu
                                                                                                                                                                                                                                                                                                  ValLeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                             GlyLysMetVal---SerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGCAACCGATATCTTCAATTCCAAAAACCTGGCTGTACAAGCCCAGAAGAAGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                                                                                                                                                                                 AAAATCACAAAGAACCTCATCAAAACAGTCATCAAGCTGGCAGTCTTGTACCGAAACAAC
                                                                                                                                                                                                                          LysLysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsn
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TVVSFYQVEYTEDRNVLSKLLAWECRELLHQVIQRHLTAKSHGRVNNVFDHFSNCEFLA
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/db_xref="LocusID:443963"
153. .722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus laevis"
/mol_type="mRRNA"
/db xref="taxon:855"
/clone="MGC:80354 IMAGE:5074412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALYNPFGPYKKHLQRLCNGVNKMLDEDNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MGC80354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Ovary, Xenopus"
/clone_lib="NICHD_XGC_Ov1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.03e-66
842.50
95.24%
84.66%
87.58%
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Matches:
Conservative:
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Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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JOURNAL
PUBMED
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                  Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
cDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kav
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 3986)
Director MGC Project.
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Danio rerio
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(cDNA clone
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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[ (bases 1 to 3986)
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Stephanie Rodrigues, Amy Sanchez and Michelle W
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                               Michelle Whiting
                                                                                                                                                                    Ko-ichi Kawakami
(LLNL)
                                                               Anuradha
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This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 41056158.
Location/Qualifiers
                                                                          GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly 143
                                                                                                                                                                                                              AspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrVal 103
                                                                                                                                                                                                                                                                                                                                                                                                                      ValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGlu
                 ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn 163
                                                                                                                                                ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn 123
                                                                                                                                                                                             GAGGAGCTAGCGTTAGTCGAGCGTTTTCGTAAGAAGGTGCATACGCTGGCGATGACAGCT
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                                                                GACTGCCGTGAACTTCTGCACCAGGCCATCAATCGGCATCTAACGGCGAAATCTCACGCC 618
                                                                                                                              GTTAGCTTCTACCAGATCGACTTCACTTTTGATCGACGCGTCATGAGTAATCTACTCAAT
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CGAATCAACCATGICTICAATCATTTCGCCGATTGTGACTTCCTCGCGACGCTATACGGA 678
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vtkeytrnrkeaqkiiknlikmvvklgvlyrngqfnnselalverfrkkvhtlamtav
sfyqldftfdrkvmskllndcrellhgainrhltaksharinhvfnhfadcdflatly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Whole body, adult, (one male including unfertilized eggs)" (clone_ib="Sugano Kawakami zebrafish DRA" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="tumor necrosis factor, alpha-induced protein_id="AAH52765.1" /db_xref="GI:31127058" /db_xref="GI:31127058"
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/db_xref="LocusID:393303"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
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                                                                                                                                             a Zebrafish BAC library
                                                                                                                              pIndigoBAC-5
                                        /db_xref="taxon:7955"
                              clone="DKEY-49M19"
                                                                                                              location/Qualifiers
                                                                                               .205949
                                                             _type="genomic
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: ZMBL; SW: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where submitted.
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Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DXEY-49M19
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                                                           Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezz
Fiedler,P., Kutter,S., Blagodatski,A., Kostov
Plachy,J., Carninci,P., Hayashizaki,Y. and Bu
Full-length cDNAs from bursal lymphocytes to
                                                                                                                        Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
   Caldwell, R.B.
Direct Submission
                                      Unpublished
                                                  function analysis
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1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
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ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn|||:::||||:::||||||||||
                                      GTGAGCTTCCACCAGATAGACTTTACGTTTGACCGCAGGGTCGTGTCAAGTGTGCTGACA
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atkbythnrkbaqkiiknlikivmklgvlyrngqfspeellvmbrfrkkvhtlamtav
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/product="hypothetical protein"
/protein_id="CAG31995.1"
/db_xref="GI:5313332"
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/mol_type="mRNA"
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/clone_lib="riken1"
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                       GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly 143
                                                                                                 GAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCATT
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           GAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGCACCTGACGCCCAGGACCCACGGG
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Yamamoto,J., Isono,Y., Nagai,K. and Iri
Full-length human cdna
Patent: EP 1440981-A 269 28-JUL-2004;
Research Association for Biotechnology
Location/Qualifiers
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                 GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly
                                                                                                                    GAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCATT
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GAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGGCACCTGACGCCCAGGACCCACGGG
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/translation="mDSDSGEQSEGEPVTAAGPDVFSSKSLALQAQKKILSKIASKTV
/translation="modSegept"/"
/translation="mo
                                                                                                                                                                                                                                                                                                                                                                                                                         note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="amygdala"
/clone_lib="BRAMY2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="BRAMY2038484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
1.04e-48
651.00
89.07%
Length:
Matches:
Conservative:
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Homo sapiens chromosome 15 clone RP11-394B5,
SEQUENCE, 10 unordered pieces.
AC012678
                                                                                                                                                          Z (bases 1 to 188937)
Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J.,
                                                                                                                                                                                                                                                                                                                           Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A. J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                              Submitted (03-NOV-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                             Direct Submission
                                                                                                                                  Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HT
Homo sapiens (human)
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                                                                                                                                                                                                            Pred. No.:
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Chemistry: Dye primer; 0% of reads
Chemistry: Big Dye Terminator; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177081 bases at least Q40
Consensus quality: 18532 bases at least Q30
Consensus quality: 186766 bases at least Q20
Insert size: 188828; agarose-fp
Insert size: 188847; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.2 in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                   ASpValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMet
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Center clone name: RP11-394B5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: hum-info@sequence.stanford.edu
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2221
7219
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                                                                                                                                                                                                                                                                                                                                                                                                Location,
                                                                                                                                                                                                                                                                        /clone="RP11-394B5"
/clone_lib="RPCI human BAC library 11"
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                            2210: CURLLY CARRY TO THE TENT OF THE TENT OF A 998 bp in length 7218: contig of 4998 bp in length 7268: gap of unknown length 15922: contig of 8654 bp in length 15972: gap of unknown length 26869: contig of 10897 bp in length 26919: gap of unknown length 39746: contig of 12827 bp in length 39746: contig of 14873 bp in length 54669: contig of 14873 bp in length 54719: gap of unknown length 6987: contig of 15178 bp in length 6987: contig of 15178 bp in length 6987: contig of 23528 bp in length 93475: contig of 23528 bp in length 93525: gap of unknown length 138958: contig of 45433 bp in length 139088: gap of unknown length 139088: gap of unknown length 138937: contig of 49929 bp in length 188937: contig of 49929 bp in length
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2220: gap of
7218: contig
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                                                                                                                                                    Length:
Matches:
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Mismatches:
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Center: Multimegabase Sequencing Center
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51934 GAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCATT
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                                                                                                                                           Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Nesbitt,R., Traicoff,R. and Hood,L.
                                                                                                                                                                                                                                                          Submitted (08-JUL-2000) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 189796)

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A. Nesbitt,R., Traicoff,R. and Hood,L.
                                                  Submitted (23-FEB-2001) Multimegabase Sequencing Center, Instit
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle,
                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of human chromosome 15 D15S146-D15S117 region
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                                                                                                                                                                                                                            (bases 1 to 189796)
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23, 2001 this sequence version replaced gi:9958002
                                                                                                                    Submission
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on,G., Kaur,A., Madan,A.,
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                                                                                                                                                                      Bloom,S.,
A., Madan,A.,
                                                        Institute
eattle, WA
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Best Local Similarity:
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68319 GCCAGCAAAACTGTGGCCAACATGTTGATGATGACACCAGCAGCGAGATCTTTGATGAG
                                                                     68199 GACTTAATCAAGGTGGCGATCAAAATCGGGATCCTCTACCGGAACAACCAGTTTAGCCAA 68140
                                                                                                                                           68259
                                                                                                                                                                          44
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                                                                                                                                                                                                                             24 ValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGlu 43
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                                                                                         LeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLys
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Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
Drafting center: SDSTDC
------ Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-394B5"
/clone="RPCI human BAC library 11"
/clone lib="RPCI human BAC library 11"
/note="Data from overlapping BACs RP11-105D1 and
RP11-522G20 were added and the consensus sequence was
determined from RP11-394B5 to the extent possible"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Overlap with RP11-522G20 AC012169"
161495. .161500
/note="low quality data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55786. .56417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="sequence data generated from subcloned PCR product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="15"
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spHisPheSerAspCysGluPheLeuAlaAlaL	171	145	S
GTCCATGAACTGGTACAGCGACACTTGACGCCCAGAACCCACGGACG	GCAAGGACCTGGTCC	32507	뮍
theumisGlnIleIleGlnArgmisLeuThrAlaLysS	luMetLeuHi	125	Ş
YrThrPheAspArgAsnValLeuSerArgL ATACCTTTGATACGAATGTGCTCTCTAAAC	SerPheHisGlnValAspT :::: AGCTTCTACGAAGTGGAGT	105 32567	B 5
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LeuileLysThrVallleLysLeuAlalleLeuTyrArgAsnAsnGlnPheAsnGlnAsp 84	LeulleLysThrVallle	32697	} &
ThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsn 64 ::: ::: ::: ACCGAAGAACACCCACAACAAGAAGGAGGCCCACAAGATCATGAAGGAT 32688	TyrArgValThrArgGluTyrTh ::: TACAAAGTCACCGAAGAACACAC	32747	B 5
erilealaThrThrLeuileaspAspThrSerSerGiuValLeuAspGiuLeu 44 ::::: 	SerLysSerlleAlaThr :::::: AGCAAAACTGTGGCCAAC	32807	유 성
GAAGATCCTGAGCAAGATAGCC 3	GTGTTTAGCTCCAAGAGT	3286	맖
ValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetVal 24 ::: ::: :::	ValPheAsnSerLysAsr ::: :::	л	Ş
AC115187_1 (1-110000)	2 (1-188) x AC115	-10-627-571-	SU
2.64e-45 Length: 110000 333.00 Matches: 109 37.91% Conservative: 51 99.89% Mismatches: 22 55.80% Indels: 0	8: 2.64e-4 633.00 ity: 87.91% 1arity: 59.89% 65.80%	Alignment Score Pred. No.: Score: Percent Similar Best Local Simi Query Match: DB:	Alic Pred Scoo Per Bes Que DB:
ragments LOCUS AC115187 Accession AC115187 location End 1 110000 1 210000 200001 310000 100001 410000 100001 420106 AC115187 from base 100001 (AC115187 Rattus norvegicus clone	to 5 f B 1 2 2 3 3 5) of	WECOMMENT Sequence split in Fragment Name AC115187 0 AC115187 1 AC115187 2 AC115187 3 AC115187 3 AC115187 4 Continuation 7 of	ი "
		RESULT 36 AC115187_1/c	E A R
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.86	18	184	Ş.
::: ::::::: ::::	GACTGTAG	67899	뫄
ProHisLeuGlnLysLeuCysAspGlyIleAsnLysMet	ProPheGlyAsnPheLys	164	Ş
	CGCATCAACCACGTCTTT	67959	ДĎ
mValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn 163	ArgValAsnAsnValPhe	144	ð
CCACGGG 6	GAGTGCAAGGACCTGGTG	68019	당 :
laLvsSerHisGlv 143	GluCvsArgGluMetLeu	124	Ş
::::: :::	GTCAGCTTCTATGAGGTG	68079	닭
sGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn 123	ValSerPheHisGlnVal	104	Ş

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                                Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwonu, G., Olampunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Reevers, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walter, B., Wang, J., Walse, R., Walter, B., Wang, J., Warren, J., Warren, R., Wei, X., White, F., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wijht, D., Wright, D., Wright, R., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
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Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.
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AC115505.4 GI:25188467
HTG; HTGS_PHASE1; HTGS_
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256285 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams, C.,
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990329
Consensus quality: 19955 bases at least Q40
Consensus quality: 203424 bases at least Q30
Consensus quality: 206379 bases at least Q30
Estimated insert size: 195822; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
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organism="Rattus norvegicus"
                                                                                       Location/Qualifiers
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3: gap of unknown length
0: contig of 32587 bp in length
0: gap of unknown length
3: contig of 1413 bp in length
3: gap of unknown length
6: contig of 1413 bp in length
6: contig of 1373 bp in length
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6: contig of 1403 bp in length
9: contig of 1403 bp in length
9: contig of 1403 bp in length
9: gap of unknown length
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                                                                                                                                                                                         contig
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gap of unknown length
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of 3249
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AC129440
AC129440.3 GI:30581254
HTG; HTGS_PHASB1; HTGS_DRAFT; HTGS_ENRICHED.
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                                                                     Rattus norvegicus clone CH230-112K14, ***, 7 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuileLysThrValileLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAsp 84
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                                                                                                                                                                                                                                                                                     ATAAACCATGTCTTCAACCACTTCGCTGATGTGGAATTCCTTTCCACTCTCTACAGTCCG
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228541. .229886
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24658. .25854
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4086. .6215
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245270. .247000
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'db_xref="taxon:10116"
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Baldwin, D., Bandaranaike, D., Barbered, M., Barnstead, M., Branchmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Berden, M., Bryant, M., Bhaby, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockeell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Andar, C., Dederich, D., Delgado, O., Deneon, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Duraper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Feater, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Harvey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Hares, S., Hladun, S. L., Hodgson, A., Hogues, M., Hellins, B., Howells, S., Hulyk, S., Hume, J., Tilebird, D., Jackson, A., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S.
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:23264293. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                          Baylor Plaza, Houston, TX 77030, 3 (bases 1 to 273225)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley,K.C.
Direct Submission
Submitted (30-JUL-2002) Human Genome Sequencing Center, Department
Submitted (30-JUL-2002) Human Genetics, Baylor College of Medicine, One
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Ben
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                 Rat Genome Sequencing Consortium.
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                                                            Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: Atlas 3.0;
Consensus quality: 224959 bases at least Q40
Centersus quality: 227786 bases at least Q30
Centersus quality: 227786 bases at least Q20
Centersus quality: 229294 bases at least Q20
Estimated insert size: 236137; sum-of-centigs estimation
Quality coverage: 6x in Q20 bases; sum-of-centigs estimation
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                                                                                                                                                                                                                                                                                 end_sequence:BH258362
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:lone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="CH230-112K14"
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db_xref="taxon:10116"
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,4942: gap of unknown length
265126: contig of 260184 bp in length
265226: gap of unknown length
266729: contig of 1503 bp in length
266829: gap of unknown length
268869: gap of unknown length
268869: gap of unknown length
26899: gap of unknown length
270127: contig of 1158 bp in length
27027: gap of unknown length
271518: contig of 1291 bp in length
271618: gap of unknown length
        6.73e-45
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87.91%
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    Genome Center

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                Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacCean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Mencus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Muyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Betterson, K., Phunkhang, P., Perre, N., Pollara, V., Pattre, M., Pollara, V., Poltara, P., Poltara, P
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
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1 (bases 1 to 164258)
Birren,B., Nusbaum,C. and Lander,E.
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Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.
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REFERENCE TITLE JOURNAL

AUTHORS

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Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McGarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McGarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wirsch, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-FEB 2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 24, 2003 this sequence version replaced gi:28261544. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: L25165
Center clone name: 174 0 15
Center clone name: 174 0 15
Center clone name: 174 0 15
Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 162666 bases at least Q40
Consensus quality: 163183 bases at least Q20
Consensus quality: 163183 bases at least Q20
                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Insert size: 163558; sum-of-contigs
Quality coverage: 11.0 in Q20 bases;
Quality coverage: 11.0 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
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29707: contig of 29707 bp in length 29807: gap of 100 bp 32340: contig of 2533 bp in length 32440: gap of 100 bp 37689: contig of 5249 bp in length 37789: gap of 100 bp 104529: contig of 66740 bp in length 104629: gap of 100 bp
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     TGCAAGGACCTGGTACATGAACTGGTACAGCGACACTTGACACCCAGGAACCCCATGGACGC 87572
                                                                                               SerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGlu 124
                                                                                                                                                                                                 GAGGTTATAATTGTGGAGAAACTCCGGAAGAAACTGAACCAGACTGCGATGACCATGGTC
                                                                                                                                                                                                                                            GluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValVal 104
                                                                                                                                                                                                                                                                                                                                                                                                                           TyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsn 64
                                          CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg 144
                                                                                                                                                                                                                                                                                                                                                                                           TACAAAGTCACAGAAATACACACCCACAACAAGAAGGAGGCCCACAAGATCATGAAGGAT 87812
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vector_side:right"
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/note="assembly_fragment"
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clone_lib="RPCI-24 Male
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db_xref="taxon:10090"
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115126: gap of 100 bp
131677: contig of 16551 bp in length
131777: gap of 100 bp
158793: contig of 27016 bp in length
158893: gap of 100 bp
164258: contig of 5365 bp in length.
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COMMENT

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RESULT 40

DEFINITION AC107848

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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gode, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, W., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., W., X., Wyman, D., Ye, W.J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
2E 3 (bases 1 to 1955/4)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Aracchchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Aracchchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fizgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachugha, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 9, clone RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Rodentia;
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus_musculus (house mouse)
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Best Local Similarity:
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Center clone name: 321_A_19
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7979
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/clone_lib="RPCI-23
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/db_xref="taxon:10090"
/chromosome="9"
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28230: gap of
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59488: contig
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103534: contig
103634: gap of
142683: contig
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154263: contig
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Vassiliev,H., Venkataraman,V.S., Viel,R., V Wyman,D., Young,G., Zainoun,J., Zembek,L., Direct Submission Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Wu, X.,

Submitted (22-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2004 this sequence version replaced gi:44886703. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Web site: http://www-seq.wi.mit.edu Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR

Contact: sequence_submissions@genome.wi.mit.edu

NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is

VERSION KEYWORDS

ACCESSION

SOURCE

ORGANISM

REFERENCE

JOURNAL

REFERENCE

AUTHORS TITLE

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

7878: contig of 7878 bp in length 7978: gap of 100 bp 28230: contig of 20252 bp in length 100 bp of 31158 bp in length

154363: gap of 100 bp 195574: contig of 41211 bp f 100 bp g of 2478 bp : 100 bp of 11480 bp in length 100 bp of 39049 bp in length 100 bp of 41368 bp in length in length in length

Female Mouse BAC"

Mismatches: Indels: Conservative: Matches: Length:

REFERENCE AUTHORS

TITLE JOURNAL

45 TyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsn 64

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160545 GACAAG 160550
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                    Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Fahey, J., Helton, E., Ketteman, M., Wadan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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Butterfield, Y.S., Krzywinski, M.I., Schmutz, J., Myers, R.M.,
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Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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IMAGE:6639647), complete cds.
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                                                                                                                                                                                                                                                                         Best Local Similarity:
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3 (bases 1 to 11.5) Klein, S. and Gerhard, D.S.
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Tissue Procurement: Martha Rebbert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project
Contact: XGC help desk
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20892-7510, USA
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83.89%
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RESULT 41 BC076797

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151 TTTAGCTCAAAGAGCTTTGCTGTTCAAGCCCAGAAGATTCTCAGTAAGATGGCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 158 Row: d Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-JUL-2004) National Institutes of Health, Xenopus Collection (XGC), National Institute of Child Health and Human
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                                        PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer
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VENERKKLNQTCMTAVSFFEKEYTFDKNVLSGLLHECKTLLHELVQRHLTPKSHSRID
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/clone="MGC:83729 IMAGE:6639647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Vector: pCMV-SPORT6.1"
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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Boutferd, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Boutferd, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                           Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1813)
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                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAATTACAGGCCGTACCTCAAAAGGATTTGTGAAGGGGTCAATAAATTACTTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAGGGTTTTAATCATTTTGCTGATGTGGAATTCCTTACTGCCCTCTATAGCCTTGAA 630
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                                                                                                                                                                                 (bases 1 to 1813)
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Best Local Similarity:
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86 LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer 105
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OR analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
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Tissue Procurement: Leonard I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dickson,
                                                                                          IleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                              AAGGCCAGTCGAGAATACACCAAGAGCAAGAAGGCAAGCCCACAAGATCATCAAAGATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein MGC63960"
/protein id="AAH53167.1"
/db_xref="G1:31418811"
/db_xxef="LocusID:393322"
/translation="MDSDGGEQSEGELSPGHESFNGKSLALQAQKKILSKMATMAVAN
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VERFKKKMNQAAMTVVSFYEYEYTFDRGILSELLLECRDLLHELVEHHLTMRSHGRID
HVFNHFADVDFLTELYGPSEDYRLNLRKICDGINKLLDEGTL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="zgc:63960"
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178. .786
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/clone_Tib="NCI_CGAP_ZKid1"
/lab_host="DHIOB"
/note="Yector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="MGC:63960 IMAGE:6791907"
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(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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1813 106 46 28 0

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354 45 294

474 85 414 25

REFERENCE AUTHORS

KEYWORDS SOURCE

ORGANISM

VERSION

RESULT 42 BC053167

DEFINITION ACCESSION

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                                                                                                                                                                                                                                                                                                                                           Center project name: zC283G6
------ Summary Statistics
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 134439 bases at least Q40
Consensus quality: 134480 bases at least Q20
Consensus quality: 134490 bases at least Q20
Insert size: 134497; sum-of-contigs
Insert size: 134497; sum-of-contigs
Quality coverage: 10.02x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
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CR407586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 134497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS PHASE2; HTGS Danio rerio (zebrafish) Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code:
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                                                                                                                                                                                                                                                                                                                               coverage: 9.90x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACCACGTTTTCAACCATTTCGCCGATGTGGATTTCCTGACCGAGCTGTACGGCCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aug 26, 2004 this sequence version replaced gi:50871872.
                                                                                                                                                                                                                        is sequence will be replaced
the finished sequence as soon as it is available and
accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rerio clone CH211-283G6,
                                  clone_end:T7
              vector_side:right"
                                               /note="assembly_fragment:00151
                                                                                                          /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CHZ11-283G6"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                            /clone_lib="CHORI-211"
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Best Local Similarity:
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                                                                                                                                          JOURNAL
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                                                                   Submitted (08-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 9, 2004 this sequence version replaced gi:52137684.
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                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 189797)
Mashreghi-Mohammadi, M.
                                                                                                                                                                                                                                                                                                                                                                       BX927313 189797 bp
Zebrafish DNA sequence from clone
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                    Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                   Danio rerio
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                                      Center code: SC
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CH211-12A1 in linkage group 18,
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During sequence assembly data is compared from overlapping clones.

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US-10-627-571-2 (1-188) x BX927313 (1-189797)
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Best Local Similarity:
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep Clone-derived http://www.sanger.ac.uk/Projects/Celegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lab, WashU). For further information see
http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-12A1
is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
ArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgVal
                                                                TTTTATGAAGTGGAGTACACATTCGACCGAGGCATTCTTTCAGAGCTGCTGTTGGAATGT
                                                                                                                                                                                       ATGGAGACAGTGGAGCGCTTCAAAAAGAAGTGAACCAGGCGGCCATGACAGTGGTGAGC
                                                                                                                                                                                                                    LeuAlaLeuMetGluLysPheLysLysUysValHisGlnLeuAlaMetThrValValSer
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                                                                                                       PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys
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/clone_lib="CHORI-211"
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/db_xref="taxon:7955"
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Conservative:
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167254 GACCACGTTTTCAACCATTTCGCCGATGTGGATTTCCTGACCGAGCTGTACGGCCCATCT 167195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W., Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Montegomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 1 Mb region in 19p13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-JUL-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. Cosmid R33729 overlaps BAC 48708 to the left from bases 1 to 8,574 and overlaps cosmid R26894 to the right from bases 26,845 to 32,360. Additional chr 19 map and sequence information are available at: http://www-bio.llnl.gov/genome/genome.html.
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complement(354..69)
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                                                                                                    /rpt_
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710. .787
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1562. .1672
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rpt_family="GC_rich"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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complement (5239. .5545)
/rpt family="AluSx"
/rpt family="AluSx"
5741. .5848
                                                                               /rpt_family="LLND."
complement(16172..16474)
/rpt_family="AluSq"
complement(16664..16716)
                                                                                                                                                                                                                                             /rpt_family="ALL... 14555)
complement(14175. .14555)
/rpt_family="LIMB7"
/rpt_family="LIMB7"
                                                                                                                                                                                                                                                                                                                                               complement (13408..13671)
/rpt family="AluSq"
complement (13674..13880)
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                                                                                                                                                                                    complement(14560. .14854)
/rpt_family="AluSx"
complement(14865. .15172)
/rpt_family="AluJo"
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/rpt_family="AluY"
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complement(11856..12145)
/rpt_family="AluSx"
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13135.
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complement (9773. .1
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                                                                                                                                                                                                                                                                                     /complement (24790. .25329)
/note="DDS similarity to overlapping ESTs:
/note="DDS similarity to overlapping ESTs:
(25329. .25201) AA477269 zu43c12.s1 Soares ovary tumor
NbHOT Homo sapiens cDNA clone 740758 3'; (401. .273); 100%
identity.-(25329. .25201) A477268 zu43c12.r1 Soares ovary
tumor NbHOT Homo sapiens cDNA clone 740758 5'; (221. .349);
100% identity.-(25061. .24842) A477268 zu43c12.r1 Soares
ovary tumor NbHOT Homo sapiens cDNA clone 740758 5';
(350. .570); 98% identity.-(24792. .25272) N33339 yw82g08.s1
Homo sapiens cDNA clone 258782 3'. Score: 925 Identity:
476/480 (99%).-(25329. .25028) AA579149 nf28a04.s1
NCI CGAP Pri Homo sapiens cDNA clone IMAGE:915054;
(134. .434); 99% identity.-(24790. .25061) AA477269
zu43c12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
clone 740758 3'; (272. .1); 100% identity.-Additional EST
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23246. .2340*
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/rpt_family="FLAM_C"
complement (18725. .18991)
/rot famil: """
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frame: 1, quality: excellent, score: 77.000"
complement (21587, .21852)
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complement(21329. .21549)
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complement (join(25250. .25329,27176. .27248,27914. .27995,
32121. .>32185)
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22943. .23243
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22809. .22929
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20269. .20558
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20087. .20262
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Matches:
Conservative:
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	Search completed: July 28, 2005, 20:50:53 Job time : 4523 secs	ch comple cime : 45	Sear Job
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161 19591	HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu	142 19532	유 성
141 19531	LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer	122 19472	
121 19471	ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu	102 19412	유 왕
101 19411	AsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMet :::	82 19352	유 성
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	AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys 61	42 19232	8 8
41 19231	LysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeu 	22 19172	DB Q9
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	US-10-627-571-2 (1-188) x AC005339 (1-32360)	0-627-57]	US-1
	61.64% Indels: 0 9 Gaps: 0	Query Match: DB:	Quer DB:

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Title:
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-USER-US10627571 @CGN 1 1 69 @runat 27072005 154721 27515 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 537, App
Sequence 14427, A
Sequence 14437, A
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Sequence 4950, App
Sequence 3908, App
Sequence 907, App
Sequence 39, Appl
Sequence 1, Appli
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Sequence 8, Appli
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Sequence 1081, App Sequence 898, App Sequence 3485, Appl Sequence 417, Appl Sequence 17, Appl Sequence 1, Appl Sequence 1, Appl Sequence 14, Appl Sequence 15, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 17, Appl Sequence 1
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SEQ ID NO 537
LENGTH: 1175
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Patent No.
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CURRENT FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 678396961 Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryl
APPLICANT: Asundi, Vinod
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26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr 45
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                                                  PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer
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Yang, Yonghong
Wehrman, Tom
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Chen, Rui-hong
Wang, Zhiwei
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Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunging
Yamazaki, Victoria
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US-09-774-528-176
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14427
LENGTH: 340
TYPE: DNA
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 ; OTHER INFORMATION: US-09-513-999C-14427
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APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6783961
GENERAL INFORMATION:
                    FEATURE:

NAME/KEY: misc_feature

TOTATION: 221

TOTAL TON: r=a
                                                                                     LOCATION: 208 OTHER INFORMATION: k=g
                                                                                                           NAME/KEY: misc_feature
LOCATION: 208
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LOCATION: 170
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OTHER INFORMATION: r=a
FEATURE:
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NAME/KEY: misc_feature
LOCATION: 139
OTHER INFORMATION: w=a
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CGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
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Best Local Similarity:
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; LOCATION: 32
; OTHER INFORMATION: y=c
US-09-513-999C-14434
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US-09-513-999C-14434
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Pred. No.:
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APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 36681
SOFTWARE: PATENT.PM
SEQ ID NO 14434
LENGTH: 252
Sequence 6176, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                 Match:
                                                                                                                                                       148
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                                                                                                                 21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAsp 35
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                                                                                                                                                                      1 MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
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Best Local Similarity:
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LENGTH: 1347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Candida albicans
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                                                                                                                                                                                                    144 ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn
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                                                                184 AspGluGluAsnIle 188
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                                  GACGATCAAACCGTA
                                                                                                                                   ProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeu
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US-09-248-796A-4950

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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO C
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 4950
I LENGTH: 2229
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-4950
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GTTTTTGAATATTTTTTG 1839
                                                                                                                              GCAĀĀĀCAĀĀĢĀĀĀCĀTGATTTGATĀĀTĀĀĀTGATTTGĀĀT----
                                                                                                                                                   ---LysLysLysValHisGlnLeuAlaMetThrValValSerPheHisGlnValAspTyr 111
                                                                                                                                                                                                                                                                                                                                                          LysLeu-----AlaIleLeuTyrArgAsn------
                                                                                                                                                                                                                                                                                                                                                                                                                      TyrThrGlnAsnLysLysGluAlaGluLysLysI]eLysAsnLeuIleLysThrVallle
                            IleIleGlnArgHisLeu 137
                                                                                                                                                                                                                                                                                                                            AATTTGCGTTCTGAGCTAGGTGATGCTATGCATATGAAAAATGATCTTTTATCGAATCTA 1611
                                                                                                                                                                                             TTGCAATTGAAATTGGATGAAATTAATGAAGATTATGAAAATCTTATGGAATTGACTCAA
                                                                                                                                                                                                                               LeuMetGluLysPhe---
                                                                                                                                                                                                                                                                                                                                                                                           TACACTCAGAAAGCCACTTCAAAAACCAAAGAATTGCTGATTTAAACAAGACAGTTTCG 155
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                                                                                         ThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGln 131
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-AATGTGATTATCAATCTAATGAATGATATTAAGAAAACATTATTGAGT 1821
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTMARE: FASTSEQ for Windows Version 4.
SEQ ID NO 3908
LENGTH: 2253
TYPE: DNA
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US-09-949-016-3908
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Best Local Similarity:
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Patent NO. 6812339
GENERRAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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                                                                                                                                                                                                                                                                     GlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGlu------
                                                                                                                                                                                                                                                                                                                                                                   -----PheLysLysLysValHisGlnLeuAlaMetThrVal-----ValSerPheHis 107
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                                                                                                                                                                                                                                                                                                                             GACATTGTTCGATACAGGGTGTATGAGCTAATTATAGAGATTTCTTCCGTGTCACCAGAA 597
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                                                                                           LeuThrAlaLysSerHisGlyArg------ValAsnAsnValPheAspHisPhe
                                                                                                                                           GAGGATGTGTTGGTCAGAGCCACCTGTATAGAAATGGTGACATCACTGGCATATACTCAT
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-----AspCysGluPheLeuAlaAlaLeuTyrAsnPro-----
                                             ---CATGGGCGACAATATCTTGCTCAAGAAGGAGTAATTGACCAAATT
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Best Local Similarity:
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US-09-976-594-907
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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 907
LENGTH: 5923
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Patent No. 6673549
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CURRENT FILING DATE: 2001-10-12
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OTHER INFORMATION: Incyte ID No. 6673549 977975.1
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                                                                                                                                                                                                                                                           CGCCTAGAAACTGTGTTTGTACCTCCTGAGAAACATGAAAAAAGAGATAATAGCTCTGAAA 255
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                         AACTTGAAG
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                                                              ThrAlaLys 140
                                                                                                                                        LeuLeuAsnGluCys------ArgGluMetLeuHisGlnIleIleGlnArgHisLeu
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                                                                                                  CTTAAGAAAAAATGTGGTGAAGACCAGGAGAAAATACACGCTCTCACATCTGAAAACACT 265
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Query Match:
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APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: USENION: NUCLEIC ACID PROBES AND TITLE OF INVENTION: UNEALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT APPLICATION NUMBER: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR APPLICATION NUMBER: 60/073,189
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SEQ ID NO 39
LENGTH: 1887
TYPE: DNA
ORGANISM: Ureaplasma urealyticum
US-09-601-198-39
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139 AlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 AlaGluLysLysIleLysAsnLeuIleLysThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 SerGluValLeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGlu
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                                                                                                                     GTTATTAATACTATTTACCAACAAAATTATAGTTTTTTATGATTTGATCAATTAAAATTA
                                                                                                                                                         ThrValValSerPheHisGlnValAspTyrThr-----PheAspArgAsnValLeu 118
                                       ACTAATTTAAAACAAAATCTAAACAAGAATATCACTAATATTGTTAAT--
                                                                           SerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThr 138
                                                                                                                                                                                                                                                                                                                    GluLeuAlaLeuMetGluLysPheLys----
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SEQ ID NO 1
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CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
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LOCATION: (84773)...(84773)
OTHER INFORMATION: n equals
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                  OTHER INFORMATION: n equals a,
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INCATION: (319226) .. (319226) OTHER INFORMATION: n equals a, NAME/KEY: misc feature OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (191995)..(191995) NAME/KEY: misc_feature LOCATION: (779455)...(779455) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (741684)..(741684) OTHER INFORMATION: n equals LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (600992)..(600992) LOCATION: (309398). (309398) NAME/KEY: misc_feature LOCATION: (713652)..(713652) LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (559241)..(559241) LOCATION: (312837)..(312837)
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Best Local Similarity:
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LOCATION: (1664854)...(1664855)
OTHER INFORMATION: n equals a,
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LOCATION: (1637998)..(1637998)
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                              LOCATION: (98170)..(98120)
OTHER INFORMATION: n equals a
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CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR PPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                 FEATURE:

NAME/KEY: misc feature

**COLTION: (84812)..(84/
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LOCATION: (84773)..(84773)
OTHER_INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals
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LOCATION: (98120)..(98120)
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LOCATION: (98266)..(98266)
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NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
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LOCATION: (312993). (312993)
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LOCATION: (312837)..(312837)
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals
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LOCATION: (309398)..(309398)
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LOCATION: (234814)..(234814)
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LOCATION: (234187)...(234187)
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LOCATION: (231980)..(231980)
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LOCATION: (191989)..(191989)
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LOCATION: (163385)..(163385)
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LOCATION: (148948)..(148948)
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LOCATION: (98343)..(98343)
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LOCATION: (234220)..(234220)
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LOCATION: (741684)..(741684)
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LOCATION: (657081)..(657081)
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LOCATION: (622708)..(622708)
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LOCATION: (600992)..(600992)
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LOCATION: (1310988)..(1310988)
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LOCATION: (1119881)..(1119881)
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals
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LOCATION: (779455)..(779455)
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LOCATION: (713652)...(713652)
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LOCATION: (682442)..(682442)
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LOCATION: (674435)..(674435)
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Sequence 8, Applicate

Patent No. 6593463

PARLENT: Chen, Li How
APPLICANT: Chen, Li How
APPLICANT: Meade, Harry M.

TITLE OF INVENTION: NOVEL MODIFIED MSP-1 NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND METHODS FOR INCREASING MRNA LEVELS AND PROTE
TITLE OF INVENTION: EXPRESSION IN CELL SYSTEMS
FILE REFERENCE: 10275-133001
CURRENT PILLING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 60/085,649
PRIOR APPLICATION NUMBER: US 60/062,592
PRIOR APPLICATION NUMBER: US 60/062,592

PRIOR FILING DATE: 1999-05-15
PRIOR APPLICATION NUMBER: US 60/062,592

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; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN (
TITLE OF INVENTION: WITH HUMAN DISEASE, ME:
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                                                                                                                     GENERAL INFORMATION: APPLICANT: VENTER, J.
                                                                                                                                                       Sequence 975, Appl
Patent No. 6812339
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LOCATION: (1)...(1142)
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RESULT 13
US-09-016-434-1081
Sequence 1081, Application US/09016434
PATENTAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                 CysAspGlyIleAsnĻysMetĻeuAspGluGluAsn 187
                                                                                                                                                                                                    AAACCTTTGGCTTGTCTGCTGTTATCCCTAGAGAGTTTCTATCCTCCTGCTCATCAGCTA
                                                                                                                                                                                                                                                                                                     HisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCys 155
                                                                                                                                                                                                                                                                                                                                                            AsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArg 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTCAGCCTTCGTGGATTTCTTCCTCTACGGAGTATTTAAACACTATCGGCAAAAAGAAG
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CLONE: GENEAUK
CLONE: 91174071
US-09-016-434-1081
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Best Local Similarity:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSER: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: CALIFORNIA
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                                                                                                                   GGCAAGAGTACGTTTATCAAGCAGATGAGAATCATCCATGGGTCAGGATACTCTGATGAA
                ValSerPheHis---
                                                    GATAAA-----AGGGGCTTCACCAAGCTGGTGTATCAGAACATCTTCACGGCC
                                                                                                                                                                                                                          GlnAsnLysLysGluAlaGluLysLysIleLysAsnLeuIle-------
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                                                                                 AspGluLeuAlaLeuMetGluLysPheLysLysUsValHisGlnLeuAlaMetThrVal
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Percent Similarity:
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Query Match:
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US-09-023-655-898
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US-09-023-655-898
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                                                                                      Alignment Scores:
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Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cocks,
                                                                                                                                                                                                                                                                            TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FORM:
COMPUTER: IBM FORM:
COMPUTER: IBM FORMS-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
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IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                               NAME: Zeller, Karen J. REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: UFFILING DATE: HEREWITH CLASSIFICATION:
                                                                                                                                                         LIBRARY:
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CLASSIFICATION:
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14175
LENGTH: 1865
TYPE: DNA
                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-270-767-14175
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US-10-627-571-2 (1-188)
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                                                                                                                                                                                                        ORGANISM: Drosophila melanogaster FEATURE:
                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                       No. .
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x US-09-270-767-14175 (1-1865)
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Matches:
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Sequence 3485, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUMBER: US/09/710,279
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
INUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3485
LENGTH: 3204
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Query Match:
DB:
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US-09-710-279-3485
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                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                            PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                  Local Similarity:
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                       23 MetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAsp
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Percent Similarity:
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Query Match:
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US-10-627-571-2 (1-188)
                                                                                                                                                                                                                            US-09-710-279-4311
                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

APPLICANT: KIMMERLY, WILLIAM JOHN

ITILE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PAtentin Ver. 2.1

SEQ ID NO 4311

LENGTH: 3627

TYPE: DNA
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                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Percent Similarity:
Best Local Similarity:
                                                                                                                          ; ORGANISM: Artificial Sequence; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4029
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                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                    Sequence 4029, Application US/09710279
PATENT NO. 6703492
GENERRAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 1090-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
PRIOR PRIOR SEQ ID NOS: 4472
                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4029
LENGTH: 3760
                                                                                                                                                                                                                             TYPE: DNA
                                                                      No.:
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39.41%
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        Length:
Matches:
Conservative:
Mismatches:
        3760
46
34
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APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: APJONA, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: AFHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US/09/99,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US/09/31,930
PRIOR APPLICATION NUMBER: US/09/31,930
PRIOR APPLICATION NUMBER: US/09/31,930
PRIOR FILING DATE: 1997-06-03
NUMBER: OF/SEQ ID NOS: 53
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Appl Patent No. 663292
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Ann M.
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                                                                                                                                                                                                                                                                                                                                           Lees,
                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09616289
                                                                                                                                                                                                                                                                                                                                             Robert S.
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  RESULT 20
US-09-750-590A-3
; Sequence 3, Application US/09750590A
; Patent No. 6780987
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (1)...(1638)
US-09-616-289-46
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SEQ ID NO 46
LENGTH: 1638
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                1207
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                                                                                       1267 AAGAAGCTGGAGAAAGAA
                                                                                                                                                                                                                                                                                                                     1030 GCCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAGCGGGAGAAGGATTTT---CTC
                                                                                                                 180 AsniysMetLeuAspGlu 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 CAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAAGGACCAC
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                                                                                                                                                                                                                                                                                                                                         CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg 144
                                                                                                                                              AAAAGCAGCGAGGTATTCACCACATTCAAGCAGGAGATGGAAAAGATGACTAAGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                      AspTyrThrPhe------AspArgAsnValLeuSerArgLeuLeuAsnGlu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSerPheHisGlnVal 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGATGGAACAGCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATGGAGCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaIleLeuTyr-----ArgAsnAsnGlnPheAsnGlnAspGluLeuAlaLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLysLysIleLysAsnLeuIleLys------ThrValIleLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLeuTyrArgValThrArg------GluTyrThrGlnAsnLysLysGluAla
                                                                                                                                                                                                                                                             CTGAAAGAGGCAGTAGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCAC 1146
                                                                                                                                                                                                                                                                                       ValAsnAsnValPheAspHisPheSerAspCysGluPheLeu--------
                                                                                                                                                                                                                                                                                                                                                                           GACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAG------GAGCATATC
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                                                                                                                                                                                                       CTGAAGCAACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACTTTTCC
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                                                                                                                                                                                                                                   -----AlaAlaLeuTyrAsnPro-----
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Matches:
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RESULT 21
US-08-979-608A-17
; Sequence 17, Application
; Patent No. 6355451
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Bos taurus
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88.00
43.46%
18.85%
9.15%
                US/08979608A
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US-10-627-571-2 (1-188) x US-09-750-590A-3 (1-4206)
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PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 09/733,818
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 25
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APPLICANT: Welch, Alice
TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL
TITLE OF INVENTION: ABNORMAL CELL MIGRATION
FILE REFERENCE: TUI-001CP
CURRENT APPLICATION UNMBER: US/09/750,590A
CURRENT FILING DATE: 2000-12-28
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                                                                                                                                                                                                                                                                                                                                            2482 ATGTCTGAAAACAATGATTTGAAAAAGACCATGAGTCATCAGTATGTGCCCCGTGAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2326 AGTAAAAATGTCAGCCGCCTGGAAACTGTGTTCATACCTCCCGAGAGACACGAAAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2218 CATGATGTAATTGTTGATGATTTGAATAAAAAGCTTTCAGAT------GTGACA
                                                                                                                                                                                                                                                                                 142 HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 AlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyrArgValThr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIle------LysAsnLeu
:::||||||::: ||| ||| ||||| :::
GAATTTGTGAAAATAAAAGATGAGAACGAAATA
                                                                                                             TTGGATAAAACCAATAGAGAATTAGTAGATGTGAAGAAGAAGTGTGAAGATATAAATCAA 263
                                                                                                                                                                                                                                                                                                                                                                                               LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATGTGGTGAA-----GACCAAGAGAAAATATATTCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGATGGCTCTGAAATCCAATATCACTGAACTTAAGAAGCAGCTGTCTGAACTTAATAAA 2445
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                                               TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn--- 180
                                                                                                                                                                                                                            CATGAAGAGATTAAAACTGCC-
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-00200
REPERENCE/DOCKET NUMBER: 10797-00200
TELECHONE: 617/542-8096
TELEPHONE: 617/542-8996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ATJONA, ANIBAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/979,608A FILING DATE: 26-No. 6355451-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lees,
                                                                                                                                                         633
     753
                                                                               693
                                                                                                                                                                                                                               573 CAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCCAGCTGGTGCAAGAAAAGGACCAC
                                       59
                                                                                                                                                                                                                                                              14 GlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIleAlaThrThr-----
                                                                                                             43 GluLeuTyrArgValThrArg------GluTyrThrGlnAsnLysLysGluAla
                                                                                                                                                                                       32 LeulleAspAspThrSerSerGluValLeu------
 GAGGAGAAGCGCAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTCAGCTG
                                     GluLysLysIleLysAsnLeuIleLys--
                                                                           GAGCTGCAGCGGCACAACCGCTCCCTCAAGGAAGAAGGTGTGCAGCGGGCCCCGGGAGGAG
                                                                                                                                                   CTGCGCGGTGAGCACAGCAAGGCCGTCCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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36.28%
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Robert S.
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Matches:
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Patent No. 6605588
GENERAL INFORMATION:
               NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lees,
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                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert S.
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                                                                                           10797-003001
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AND

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US-09-616-289-17
; Sequence 17, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                  1221 AAGAAGCTGGAGAAAGAA
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                                                                                                                                                                                                                                                                                                        GCCCAGGAGATGCTAAAGGAGGCAGAAGAAGGACCAGCGGGAGAAGGATTTT---CTC
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                                                                                                                                        AAAAGCAGCGAGGTATTCACCACATTCAAGCAGGAGATGGAAAAGATGACTAAGAAGATC
                                                                                                                                                                                                                                                                           ValAsnAsnValPheAspHisPheSerAspCysGluPheLeu--------
                                                                                                                                                                                                                                                                                                                                  CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg 144
                                                                                                                                                                                                                                                                                                                                                               GACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                        AspTyrThrPhe------AspArgAsnValLeuSerArgLeuLeuAsnGlu 124
                                                                                                                                                                                                                                                                                                                                                                                                                     GAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAG------GAGCATATC
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                            CTGAAGCAACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCC
                                                                                                                                                                                                                    -----AlaAlaLeuTyrAsnPro-----
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Matches:
Conservative:
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Indels:
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
CURRENT PROPERICE: 10797-004001
CURRENT PHILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4697
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; NAME/KEY: CDS
; LOCATION: (3).
US-09-616-289-17
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          873
                                                                                                                                                                                                                                                                                                                                                                          813 CAGATGGAACAGCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATGGAGCTGGCT
                         145
                                                                           984 GCCCAGGAGATGCTÀAAGGAGGCAGAAGAGCGGCACCAGCGGGAGAAGGATTTT----CTC 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 GAGCTGCAGCGGCACAACCGCTCCCTCAAGGAAGAAGGTGTGCAGCGGGCCCGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 CTGCGCGGTGAGCACAGCAAGGCCGTCCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              573 CAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAAGGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 GluLysLysIleLysAsnLeuIleLys------ThrValIleLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 GluLeuTyrArgValThrArg------GluTyrThrGlnAsnLysLysGluAla 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 LeuIleAspAspThrSerSerGluValLeu------Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIleAlaThrThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                      73 AlaIleLeuTyr-----ArgAsnAsnGlnPheAsnGlnAspGluLeuAlaLeuMet 89
GluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSerPheHisGlnVal 109
                                                                                                                                                                                                                                                                          GAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAG--
                                                                                                                      CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg
                                                                                                                                                                          GACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCAG
                                                                                                                                                                                                                         AspTyrThrPhe-------AspArgAsnValLeuSerArgLeuLeuAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGAGAAGCGCAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTCAGCTG
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Percent Similarity:
Best Local Similarity:
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APPLICANT: Welch, Alice
APPLICANT: Welch, Alice
APPLICANT: Welch, Alice
TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL AND
TILE REFERENCE: TUI-001CP
CURRENT APPLICATION NUMBER: US/09/750,590A
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/170,182
PRIOR APPLICATION NUMBER: 09/733,818
PRIOR APPLICATION NUMBER: 09/733,818
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-627-571-2 (1-188) x US-09-750-590A-1 (1-4730)
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SOFTWARE: FRASLSEQ for Windows Version
SEQ ID NO 1
LENGTH: 4730
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ORGANISM: Bos taurus
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LOCATION: (39
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                    102 ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu
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                                                                                                                                                         AGTAAAAATGTCAGCCGCCTGGAAACTGTGTTCATACCTCCCGAGAGACACGAAAAAGAA
                                                                                                                                                                                                   IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                                                CACAAATATACAGAAAAGAAGTTGGAAAATGGAGAAGTTGCTTATGGAAAATGCCAGTTTA
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                                                                     ATGATGGCTCTGAAATCCAATATCACTGAACTTAAGAAGCAGCTGTCTGAACTTAATAAA
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                                                                                                             ----LysPheLysLysLysValHisGlnLeuAlaMet 101
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Gaps:
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte
US-09-976-594-940
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Patent No. 6673549
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NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REFERENCE: PA-0041 US CURRENT APPLICATION NUMBER: US/09/976,594 CURRENT FILING DATE: 2001-10-12 PRIOR APPLICATION NUMBER: 60/240,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Furness, Michael APPLICANT: Buchbinder, Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                    1311 GATTTCCTGAAAGCTCAGCAAAAATACACCAACATTGTTAAAGAAATGAAAAGCAAAGGAT 1370
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104 ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn 123
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                                                                                                                                                                            64 AsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGln
                                                                                                                                                                                                                                                                  45 TyrArgValThrArgGluTyrThrGlnAsnLys---LysGluAlaGluLysLysIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGAAATCAGGATACACAAGAAGAAAAAATGTGAAATTTATCGGAGACTGAGAGAGTTT 1430
                                                                                                                                                                                                                        GTAGTCAACCTTCTCCGCATGACTCAAATCAAAATTGATGAAAAGGAACAAAAGTCCAAG
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                                                                                      AspGluLeuAlaLeuMetGluLysPheLysLysUysValHisGlnLeuAlaMetThrVal 103
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Qy 4 AspValPheAsnSerLysAsnLeuAlaValGlnLysLysIleLeuGlyLysMet 23	RESULT 26 US-09-336-447A-2 US-09-336-447A-2 Sequence 2, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION: APPLICANT: HANGEN, ERIC J. APPLICANT: ACBI, CHRISTOPH APPLICANT: COPE, LESLIE D. APPLICANT: MACTUER, 150BEL APPLICANT: PISKE, MICHAEL J. APPLICANT: PISKE, MICHAEL S. FILE REFERENCE: AMCY:024 CURRENT FILING DATE: 1399-06-21 NUMBER OF SEQ ID NOS: 98 SOFTWARE: PATENTIAN Ver. 2.1 SEOTUALE: PISKE, MICHAEL S. LENGTH: 3349 SOFTWARE: PATENTIAN VER. 2.1 LENGTH: 3349 SOFTWARE: PATENTIAN VER. 2.1 ENGRY S. ALIGHMENT SCOTES: BYOUR S. BYOUR S. AND	Qy 182MetLeuAspGluGluAsnIle 188 ::::: ::: Db 1728 AACACGATCACAATGATCGAAGAGGAGATGGTG 1760	Qy 171 HisLeuGlnLysLeu	Qy 151 HisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPheLysPro 170	Qy 138ThralaLysSerHisGlyArgValAsnAsnValPheAsp 150	Qy 124 GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeu 137 ::: ::::::::: ::	:::
Alignment Scores: Pred. No.: 87.50 Score: 87.50 Percent Similarity: 40.36% Percent Similarity: 21.08% Mismatches: 66 Query Match: 9.10% Indels: 67 DB: US-10-627-571-2 (1-188) x US-09-952-267B-2 (1-3349) Qy 4 AspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMet 23	Oy 165 PheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeu 183	Qy 151	Qy 132 IleIleGlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAsp 150	Qy 112 ThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGln 131	Qy 106 PheHis	Qy 89MetGluLysPheLysLysValHisGlnLeuAlaMetThrValValSer 105	Db 1503 GATGATGTTGCTGACAACCAAGATGACATTGCTAAAAAACAAAGCTGACATCAAAGGTCTT 1562

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RESULT 28
US-08-979-608A-14
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                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lees, Ann M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCAAAAA 1883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTAATTCACTTCATGATGTTACTGACAACCAACAAGATGACATCAAAGAGCTTAAGAGG 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGluGlu 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACAACAGCAAGATCAGCATAGCTCTGATATCAAAAACACTT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCATGATGATGTTGCCACCAACCAAGCTGACATTGCTAAAAACCAAGCGGATATCAAA 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgAsnAsnGlnPheAsnGlnAspGluLeuAlaLeu----------
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                                                                                                                                                                                                                                                                     STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGln 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAAGGAGGTGAAAGAGCTTGATAAGGAGGTGGGTGTATTAAGCCCGAGACATTGGTTCA 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGATGTTGCTGACAACCAAGATGACATTGCTAAAAACAAAGCTGACATCAAAGGTCTT 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysileLysAsnLeuileLysThrValileLysLeuAla-----IleLeuTyr 76
                  APPLICATION NUMBER: US 60/048,547 FILING DATE: 03-JUN-1997
                                                                                                                                                                                                                                ZIP: 02110-2804
                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheGlyAsnPheLysProHisLeuGlnLys---LeuCysAspGlyIleAsnLysMetLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PheHis-----GlnValAspTyr--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACACTTGAAAACAATGTCGAAGAAGAATTATTAAATCTAAGCGGTCGCCTGCTTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----MetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer 105
APPLICATION NUMBER: US 60/031,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --AAAAACAATGTCGAAGAAGGTTTATTGGATCTAAGCGGTCGCCTCATT 1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AAAGCGGATATTGATAATAACATCAACAATATCTATGAGCTG 1784
                                                                                                                                                                                                                                                                                                                                                                                        TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---HisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnPro 164
                                                                                                                                   2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-979-608A-14
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1309
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                 139 AlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                        104 ValSerPheHisGlnValAspTyrThrPhe------AspArgAsnValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901 CTCAACGACATTCAGCTGCAGATGGAGCAGCAACGAGCGCAACTCCAAGCTGCGCCAG
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AAGATGACAAAGAAGATCAAGAAGCTGGAGAAAGAG 1344
                                  LysLeuCysAspGlyIleAsnLysMetLeuAspGlu 185
                                                                          TTCCAGAACACTCTTTCCAAAAGCAGCGAGGTGTTCACCACATTCAAACAGGAAATGGAA 1308
                                                                                                                                                   AAGCAACAGGAGACCCACCTGAAGCAGCAGCTTGCCCTATACACAGAGAAGTTTGAGGAG
                                                                                                                                                                                                                              GAGAAGGACTTT----CTCCTGAAGGAGGCCGTGGAGTCCCAGAGGATGTGCGAGCTGATG
                                                                                                                                                                                                                                                                                                         GACGCCAAGCTCCAGCAGGCCCAGGAGATGCTGAAGGAGGCAGAGGAGCGGCACCAGCGG 1131
                                                                                                                                                                                                                                                                                                                                              SerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThr 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCAGGAGAAGGACCACCTGCGTGGCGAGCACAGCAAGGCCATCCTGGCCCGCAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAACATGGAGCTGGCCGAGCGGCTCAAGAAGCTGATTGAGCAGTACGAGCTGCGAGAA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnAsnLysLysGluAlaGluLysLysIleLysAsnLeuIleLys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4722 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                    ----GAGCACATCGACAAAGTCTTCAAACACAAGGATCTGCAGCAGCAGCTGGTG 107
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36.79%
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9.10%
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                                                                                                                                                                                        -----AlaAlaLeuTyrAsnPro------
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                                                                                                           ----PheGlyAsnPheLysProHisLeuGln
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US-09-517-849-14
                                                                                                                                                                                                                 US-10-627-571-2 (1-188)
                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                               US-09-517-849-14
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GENERAL INFORMATION:
APPLICANT: Lees,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                        Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAN: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOPTWARE: FASESSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/979,608 FILING DATE: 26-NOV-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                              721
                                                                     33 IleAspAspThrSerSerGluValLeuAspGluLeuTyrArgValThrArgGluTyrThr 52
                                                                                                                                                                            13 ValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIleAlaThrThrLeu 32
                GTGCAGGAGAAGGACCACCTGCGTGGCGAGCACAGCAAGGCCATCCTGGCCCGCAGCAAG
CAGCGAGCCCGAGAGGAGGAGGAGÁAGCGCÁAGGAGGTGACGTCACACTTCCAGATGACG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4722 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 61...1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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Lees, Robert S.

Law, Simon W.

Arjona, Anibal A.

Arjona, NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING

TREATING ATHEROSCLEROSIS
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87.50
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Matches:
Conservative:
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Indels:
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APPLICANT: Law, Simon W.

APPLICANT: APJONA, ANIBAI A.

APPLICANT: APJONA, ANIBAI A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: APHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547
                  Percent Similarity:
Best Local Similarity:
Query Match:
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SEQ ID NO 14
LENGTH: 4722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09616289 Patent No. 6632923
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Oryctolagus c
FEATURE:
NAME/KEY: CDS
LOCATION: (61)...(1731)
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NUMBER OF SEQ ID NOS: 53
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                                                                                                               No.:
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Law, Simon W.
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                                                                                        Pred. No.:
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US-09-541-782-5
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                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 4223
TYPE: DNA
TYPE: DNA
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      Query Match:
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                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Wil
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09723820 Patent No. 6468760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/723,820 CURRENT FILING DATE: 2000-11-28 PRIOR APPLICATION NUMBER: 09/541,782 PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                TYPE: DNA
ORGANISM: S.pombe
                                                                                                                                                                                                                                LENGTH: 4223
                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3107 GCAGATATAATATTAAGTGATTACATATCTGATCAAAAATCCAAATTTGAATCCAAGCAA 3166
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    Query Match:
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US-10-270-085-5
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                                            Percent Similarity:
                                                                     Score:
                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/10270085
Patent No. 6627408
                                                                                                                                                                                                                                        SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/270,085
CURRENT FILING DATE: 2002-10-11
                                                                                                                                                                                           LENGTH: 42
TYPE: DNA
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/541,782 PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/723,820
PRIOR FILING DATE: 2000-11-28
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                                                                                                                          Alignment Scores:
                                                                                                                                                                       US-09-248-796A-4746
                                                                                                                                                                                                             SEQ ID NO 4746
LENGTH: 2469
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4746, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                         ORGANISM: Candida
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Query Match:
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; LOCATION: (3),(29),
; OTHER INFORMATION:
US-09-248-796A-5857
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                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 5857
LENGTH: 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5857, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-248-796A-5857
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                               ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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APPLIANCE DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1B024-US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08462949
Patent No. 5606022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TITLE OF INVENTION:
                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
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VENTION: Cloning and Identification of a Two
VENTION: Component Signal Transducing Regulatory
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DB:
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2651 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
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                                                                                                                          1171 CTTGAACTCGTGTGTCATATTGTTGATAAAGTCATTCTTCATTTC----TGTCAGCTT 1118
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                                                              CTTCTGGCG 1109
                                                                                              LeuAlaAla 160
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Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
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; GENERAL INFORMATION:
; APPLICANT: RASMUSSEN
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/023,764B
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,658-00
TRLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (201)831-33(
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 15
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LENGTH: 2651 base pairs
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American Cyanamid Company
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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TELEFAX: (201)831-3305
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                                                                                     LysPheLysLysValHisGlnLeuAla--
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Component Signal Transducing Regulatory
Bacteroides Fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                         ----AsnGlnAspGluLeuAlaLeuMetGlu
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-MetThrValValSerPheHis :::||||::::::::||||||
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Enterococcus faecalis US-09-134-000C-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACITITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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US-09-134-000C-1489
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SEQ ID NO 1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                     LysLysGluAlaGluLysLysIleLysAsnLeuIleLysThrValIleLysLeuAlaIle
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Alignment Scores
                                      ; CELL TYPE: PCT-US94-01101-1
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APPLICANT:
                                                                                                                                                                                                                                                                       TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/
FILING DATE: FILED HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B081
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TITLE OF INVENTION: FAC-
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREEN
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
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                                                                           ORIGINAL SOURCE:
ORGANISM; HOM
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                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                  ANTI-SENSE:
                                                                                                                                  HYPOTHETICAL:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-949-016-5562
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      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5562
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                                                                                                                                                                                                                                                                                                     Sequence 5562, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Matches:
Conservative:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                Sequence 636, Application Patent No. 6812339
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TYPE: DNA
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Best Local Similarity:
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US-09-949-016-636
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: LENGTH: 10300
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GENERAL INFORMATION:

APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                         Sequence 1541, Application Patent No. 6380370
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                                                                                                                            Sequence 84, Application US/09404879A

Patent No. 6468546

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS:
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF CONTRACTOR NO. 2007
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                   US-09-404-879A-84
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                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 84
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LENGTH: 2637
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TYPE: DNA
                                TYPE: DNA ORGANISM: Homo sapien
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                                                                   LENGTH: 571
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                                                                                                     FastSEQ for Windows Version
                                                                                                                                                                                      COMPOSITIONS AND METHODS FOR DIAGNOSIS OF OVARIAN CANCER
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US-10-627-571-2 (1-188) x US-09-134-001C-1541 (1-2637)
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GENERAL INFORMATION:

ARPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: King, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI

TITLE OF INVENTION: OVARIAN CANCER

FILE REFERENCE: 210121.462C1

CURRENT APPLICATION NUMBER: US/09/338,933

CURRENT FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 312

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 84

LENGTH: 571
   Alignment Scores:
Pred. No.:
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Best Local Similarity:
Query Match:
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                                                                                        TYPE: DNA
ORGANISM: Homo
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APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO.
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION MUMBER: US/09/215,681A
CURRENT APPLICATION MUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOPTWARE: FRESEQ for Windows Version 3.0
SEQ ID NO 84
LENGTH: 571
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 84, Application US/09215681A Patent No. 6528253
                                                                                                                         ORGANISM: Homo sapien
                                                                                                                                             TYPE: DNA
                                                       No.:
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Match: 8.78% Indels: 33 Gaps: 8 627-571-2 (1-188) x US-09-215-681-84 (1-571) 7 AsmSerLysAsmLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLys 26	Qy 176 Db 31	Oy 156 Db 88	Qy 136 Db 112	Qy 117 Db 172	Qy 97 Db 211	Qy 81 Db 271	Qy 61 Db 325	Oy 43 Db 385	Qy 27 Db 445	Qy 7 Db 505	US-10-627-571	Query Match: DB:
Indels: 33 Gaps: 8 Gaps: 8 31 32 33 34 35 36 36 36 31 31 31 32 31 32 32 32 32 32	CysAspGlyIleAsnLysMetI ::: AGTAACTCTTTAGAAAAATGTI	GluPheLeuAlaAlaLeuTyr/ GAATTAGCTAAGTTGGAA	HisLeuThrAlaLysSerHis(CACCTATAC	ValLeuSerArgLeuLeuAsn(HisGlnLeuAlaMetThrValV GAGTCCAAGGCCCAGACAGAGG	PheasnGlnaspGluLeuAlai ::: :: aTCCATATGGAAGAATTAAAG	LysIleLysAsnLeuIleLys' ::::: AGACTCAAAGAAGATAATTGC	GluLeuTyrArgValThrArg aagcTaagaaaTgggagagg	SerIleAlaThrThr	AsnSerLysAsnLeuAlaValo	-2 (1-188) x US-09-215	8.78 % 4
33 8 8 8 8 8 8 8 8	LeuAspGlu 185 ::::: AAGGAACAA 2	AsnProPheGlyAsr ::: CAGAACTTAAGAGI	3lyArgValAsnAsr	31uCysArgGluMet ::: ::: 3AAAACAAAGAACTT	ValSerPheHisGlr 3TCCAGCTTCAGCAC	Leu : : : ATTAACATTTCCAGO	ThrVallleLysLet ::: ::: aGTGTTCTAAAGGA1	31uTyrThrG1n :::::::: AAGTTTAGTGATGCC	LeuIleAsp ::: ATGTCTTCCCTCCAC	GlnAlaGlnLysLys aGCAACTTCAGGA/	-681-84 (1-571)	Indels: Gaps:
26 3 4446 60 60 7 326 7 326 1 113 1 115 1 115 1 115 1 115		PheLysProHisLeuGlnLysLeu 	\ValPheAspHisPheSerAspCys CACAGTTCTCAGAAT	LeuHisGlnIleIleGlnArg 	.spTyrThrPheAspArgAsn	MetGluLysPheLysLysVal ::: ::: CTTGAACATGACAAGCAGATTTGG	\AlaIleLeuTyrArgAsnAsnGln ;;; CAACTTAGACAGATGTCC	AsnlyslysGluAlaGluLys)AspThrSerSerGluValLeuAsp GATGATCGTGACAGGGTGATAGAT			8 3 3

Search completed: July 28, 2005, 19:39:58 Job time : 1080 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-[cgn2_1/USPTO_gpo2_lh/US10627571/runat_27072005_154719_27497/app_query.fasta_1.327
-Q=[cgn2_1/USPTO_gpo2_lh/US10627571/runat_27072005_154719_27497/app_query.fasta_1.327
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DCALIGN=200 -THR_SCONE=pct -THR_MAX=100 -THR_MN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US10627571 @CGN 1 1_470 @runat_27072005 154719 27497 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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Perfect score:
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Ada63216 Human gen
Ada631180 Movel human
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The invention relates to a novel method for identifying a compound that modulates T lymphocyte activation. The method comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound, where the A-raf-1 or TCPTP/PTPN2 polypeptide is encoded by a nucleic acid that hybridises to a nucleic acid encoding a polypeptide having a
                                                                                                                                   Identifying a compound that modulates T lymphocyte activation, useful for monitoring changes in cell surface marker expression, comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPNZ polypeptide with a compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTDN2; asthma; immunosuppressive; antiasthmatic; antiallergic; antiinflammatory; lymphocyte activation; lymphocyte migration; cytokine production; cell surface marker expression; antibody production; apoptosis; allergy; antibody proliferation; antibody differentiation; hypersensitivity; graft versus host disease; inflammation; gene; ss; TNF-induced protein;
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                                                                                                    Disclosure; Page 84; 126pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has cid immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory cactivity. The method is useful for identifying compounds that modulate lymphocyte activation and migration, and for monitoring changes in cell surface marker expression, cytokine production, antibody production, compounds that modulate cytokine production, antibody production, compounds that suppress or activate in and as a compounds that suppress or activate lymphocyte compounds that suppress or activate lymphocyte conduction and digration, e.g. for the treatment of diseases in which modulation of the immune response is desired such as delayed type cand acute and chronic inflammation. Modulators of lymphocyte activation and migration. The present sequence is used in the exemplification of the immune response related T and B cell activation and migration. The present sequence is used in the exemplification of the invention
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                    standard;
                                                                                                  LysMetLeuAspGluGluAsnIle
                                                                                                                                                                     LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                             New SCC-S2 polypeptides and nucleic acids encoding them, useful as target for identifying compounds that modulate cancer progression inhibiting apoptossis, as a target for detecting cancers, or for immunizing animals.
                                                                                                                                                                                                                      No.:
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                                                                                                                                                      Ota T,
Ishii
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                                                                                                                                                                                                                                                                                                                               Isogai T,
Sugiyama
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; antisense therapy;
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A, Nagai
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C, Otsuki
                                                                                                                                                                                                                                                                                                                                        Yamamoto T;
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The present invention describes primer sets for synthesising 56 length cDNAs defined in the specification. Where a primer set c (a) an oligo-dT primer and an oligonucleotide complementary to complementary to a polynucleotide which comprises one of

sequences defined in the

specification, where

one of

Claim

8;

SEQ ID

NO 12751;

2537pp +

Sequence Listing;

English

5602

comprises: fullPrimer sets for synthesizing polynucleotides, particularly the 5602 ful length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

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Best Local Si
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end cCC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence') -end sequence is selected from those defined in the CC specification. The primer sets can be used in antisense therapy and in CC gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH19742 represent human cDNA sequences; AAB92446 to AAB95893 CC present human amino acid sequences; and AAH13632 represent CC consent invention.
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                        LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn 180
                                                                                                                                                                                        SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
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                                                                                                                                                                                                                                                   CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
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AAAATGTTGGATGAAGAGAACATA 703
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99.47%
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AAH14793 ID AAH1

AAH14793 standard; cDNA; 1729

S

US-10-627-571-2 (1-188) x AAH14793 (1-1729)

MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu

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Percent Similarity:
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Query Match:
DB:
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(C (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in the

CC polynucleotide comprises are useful for synthesising polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC garticularly full-length cDNAs. The primers are also proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC CDNAs easily without any specialised methods. AAH03166 to AAH13528 and

CC CDNAs easily without any specialised methods. AAH03166 to AAH13528 and

CC CDNAs and AAH1342 represent human cDNA sequences; ABB92446 to AAB95893

CC present human amino acid sequences; and AAH13629 to AAH13632 represent

CC considered to a constant of the constant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                 Sequence
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CC gastrointestinal-Gen, antiastimatic, antiarreriosclerotic, communomodulator, cerebroprotective, vasotropic, immunosuppressive or cc vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an cc immune disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder and inflammatory disorder. The condition is an cc immune disorders, Hodgkin's lymphomas, haematopoletic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell curvival, evasion of immune responses, rheumatoid arthritis, inflammatory cowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick cyndrome, stroke, EAR, autoimmune disorders, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, corgan transplant rejection, conditions related to organ transplant cejection, conditions related to organ transplant conditions birth defects, necrotic lesions, wounds, cr jection, disorders related to aberrant signal transduction, problem of the novel association with the NF-kappaB pathway of the commendation and the novel association with the NF-kappaB pathway of the commendation of the organ transplant association with the NF-kappaB pathway of the commendation of the organ transplant association with the NF-kappaB pathway of the commendation of the organ transplant association with the NF-kappaB pathway of the commendation of the organ transplant association with the NF-kappaB pathway of the commendation of the organ transplant association with the NF-kappaB pathway of the commendation of the organ transplant association with the NF-kappaB pathway of the commendation of the organ transplant association with the NF-kappaB pathway of the commendation of the organ transplant a
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Sequence 1814 BP;
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590 A; 297
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   372 G; 555
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                                                                                                                                                          174 GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAGATCTTG
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                                                                                                                                                                            1 MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
                                                            LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                  GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG
                                                                                                                 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                        CTGGACGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer; HIV propagation; gene; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infeccion; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or
                                                                                                                                                                                                                                                                                                                           14-JAN-2003; 2003US-0440068P.
12-MAY-2003; 2003US-0469757P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
                                                                                                     P-PSDB; ADR14217.
                                                                                                                                   WPI; 2004-562168/54.
                                                                                                                                                                                                 Nadler SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NF-kappaB pathway-associated gene SeqID217.
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                                                                                                                                                                                                                                                                (BRIM )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654
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                                                                                                                                                                                                                                                                BRISTOL-MYERS SQUIBB CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAATGTTGGATGAAGAGAACATA 737
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                                                                                                                                                                                                 Neubauer MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                 Feder JN,
                                                                                                                                                                                                 Carman
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diseases associated with NF-kappaB pathway.

Claim 1; SEQ ID NO 217; 237pp; English.

CC gastrointestinal-Gen, antiastematic, antiarrents, communomodulator, cerebroprotective, vasotropic, immunosuppressive or confinement of the condition of the conditions and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The conditions is an immune disorder, an inflammatory disorder, an inflammatory disorder and immune disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM conditions, the conditions, the conditions, the conditions, hypothesis, concerns dysplasia, immunodeficiency, viral infections, HTV-1, HTV-1, heapatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAR, autoimmune disorders, disorders related to hyper compan transplant rejection, conditions birth defects, necrotic lesions, wounds, corgan transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant acute phase responses, paranting disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the conditions of the indexer from Genbank. This invention relates to the novel association of protein sequences the genes which encode them) to the NF-kappaB pathway. The invention be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

Sequence 2003 BP; 667 A; 324 C; 406 G; 606 T; 0 ς; 0 Other;

DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
13	98.75%	98.94%	99.47%	950.00	1.27e-97	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
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US-10-627-571-2 (1-188) x ADR14216 (1-2003)

160	SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160	141	8
623	CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG	564	рь
140	LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys 140	121	Ş
563		504	В
120	MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg	101	8
503	TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAAGA	444	밁
100	PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla	18	Ş
443	ATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAG	384	탕
80		61	Ş
383	CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG	324	문
60	LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys	41	Ş
323		264	당
40	GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal	21	Ş
263	GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG	204	망
20	MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu 20	1	Ş

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Query Match:
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                                              US-10-627-571-2 (1-188)
                                                                                                                                                                                                      The present invention relates to novel DNA and protein sequences which care associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vi) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) for diagnosing carcinoma; (viii) for neutralizing the effect of CAP; (vii) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma hasociated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This patent is an equivalent to basic patent
                                                                                                                                                                                Sequence 2034
                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-328604/31
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                                                                                                                                                                                                                                                                                                                                                                                                                     1; SEQ ID NO 497; Opp; English.
LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIlcAsn 180
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                                                                                                                                                                                                                                                       immunosuppressive; vulnerary; gene therapy; immune disorder; inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; hasematopoietic tumour; hyper-1gM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTIV-1; hepatitis B; hepatitis C; EBV; influenza, viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; aberrant signal transduction, poraliferating disorder; cancer; HIV propagation; gene; ds; human.
13-JAN-2004; 2004WO-US000798.
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antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2081 BP; 668 A; 359 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to the novel association of protein sequence the genes which encode them) to the NF-kappaB pathway. The invention be useful for the production of compounds with an antiinfilamatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 39; 237pp; English.
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                            The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vi) for treating carcinoma; (vii) for neutralizing the effect of CAP; (vi) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 496; Opp; English.
                                                                                                                                                                                                                                                                                                     Recombinant comprises a
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Sequence 58723 BP; 16891 A; 11477 C; 12539 G; 17816 T; 0 U; 0 Other;

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                                                                                                                                                               Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; ss.
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                                                                                                                                                                                                                                                                                                                                             by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences given in ANA97907 to ANA97915 and ANY36223 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX99916 to AAX98029 represent 110 isolated human secreted protein genes. AAY36224 to AAY36727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g.
                                                                                                                                                                                                                                                                                                         Sequence 1943 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 330; 537pp; English.
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P-PSDB; AAY36321.
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Kyaw H, Wei
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              LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
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identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polypucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present sequence represents cDNA encoding a novel human secreted protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at The invention relates to an isolated HKABT24 nucleic acid molecule. The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders. The nucleic acids are also useful for chromosome New secreted HKABT24 nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting Sequence 1943 Claim 1; P-PSDB; ADA11694 seqdata.uspto.gov.uk/sequence.html?DocID=20030055236. SEQ ID NO BP; 629 98; A; 325 118pp; ç English. 399 G; 586 Η, 0 U; 4 Other;

Query Match: DB: Percent Similarity: Best Local Similarity: US-10-627-571-2 (1-188) x ADA11570 Alignment No.: 2.06e-97 948.00 98.94% 98.94% 98.54% 9 (1-1943) Length:
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CC diagnosing, treating or preventing e.g. immune disorders, or inflammatory CC conditions, respiratory disorders, cancers, CNS disorders, or conditions, respiratory disorders, comparisoners, or conditions, respiratory disorders, comparisoners, or considers, or neurodegenerative disorders, or polypeptides comprising an amino acid compositions or antibody fragments that bind to the polypeptides, nucleic cacids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune compositions for diagnosing, treating or preventing an e.g. immune compositions for conditions (e.g. inflammatory bowel disease, comphritis or Crohn's disease), respiratory disorders (e.g. asthma and compositions or ischaemic brain injury), neurodegenerative conditions or ischaemic brain injury), neurodegenerative constructives or ischaemic brain injury), neurodegenerative conspiratory disorders (e.g. arkbrosochesis or myocarditis). The polypeptides are useful for chromosome identification, chromosome compiling, for controlling gene expression through triple helix formation or antisense DNA or NNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization composes. The polypeptides are useful for as molecular weight markers on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory disorder; cancer; CNS disorder; neurodegenerative disorders; inflammatory bowel disease; nephritis; Crohn; s disease; asthma; allergy; multiple sclerosis; ischaemic brain injury; Parkinson's disease; Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping; triple helix formation; antisense gene therapy; forensic biology; ds;
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P-PSDB; ADA57137.
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                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 592 new human secreted polypeptides useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 21; SEQ ID NO 430; 1754pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to a gene encoding one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                     LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
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                                                                                                                                                                                                                      LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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                                                                                                                                                                                                                                                                                    MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                                                                                                                                                                                                                                  TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAAGTTCATCAGCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity:
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                  MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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ATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGG
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Alignment
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                                                             Sequence
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Percent Similarity:
Best Local Similarity:
Query Match:

2.97e-9 920.00 98.94% 94.15% 95.63%

Gaps:

Mismatches: Indels:

62231 177 9 2 0

Score:

Pred.

Мо. :

.97e-92

Length: Matches: Conservative:

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ID AAH07
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  Ota T,
Ishii S,
                                                            29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                              Human cDNA clone (5'-primer)
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                                                                                                                                      28-JUL-2000; 2000EP-00116126
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  Isogai T,
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  Nishikawa T,
T, Wakamatsu
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  Saito K,
Otsuki
              Yamamoto
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WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 fullength cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 1; SEQ ID NO 4238; 2537pp + Sequence Listing; English

CC length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 cc nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence'3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in the comprises are useful for synthesising polynucleotides, comparationally full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13631 to AAH13627 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent consideration of the co invention invention describes primer sets for synthesising 5602 full-

Sequence 816 BP; 262 A; 155 Ç 180 ဌ 212 Ţ, 0 u; 7 Other;

Query Match: Percent Similarity: Best Local Similarity: Score: 2.81e-94 916.00 97.89% 96.84% 95.22% Length:
Matches:
Conservative: Gaps: Indels: Mismatches: 816 184 2 2 2 0

US-10-627-571-2 (1-188)x AAH07403 (1-816)

121	101	81	61	41	21	1
461	401	341	281	221	161	101
1 LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys 140	MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg	PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAla	LysīleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln	41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys 60	GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal	MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
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              The invention relates to a nucleic acid probe for measuring human gene CC expression, comprising any of the 27,400 fully defined nucleotide CC sequences in the specification, or their complements or fragments, and CC encoding at least 8 amino acids of any of the 6888 amino acid sequences (CC hybridises under high stringency conditions to a nucleic acid molecule (CC expressed in human cells or tissues. Also included are a spatially—CC addressable set of single exon nucleic acid probes for measuring human (comprising a plurality of single exon nucleic acid (CC probes cited above, where each of the plurality of probes is separately CC and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a wector comprising at least 8 (CC contiguous amino acids of any of the above—mentioned amino acid (CC sequences (optionally with conservative amino acid substitutions), an constant destring to measure gene expression acid substitutions), an customer desiring to measure gene expression, a method of constant and accordant of providing constant destring to measure gene expression, a method of providing and/or licensing single exon probes or microarrays to constomer desiring to measure gene expression, a method of providing constant gene expression data by subscription, and a computer-readable constant gene expression data by subscription, and a computer-readable constant gene expression data by subscription, and a computer-readable exon probe methods and apparatus are useful in cene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 22914; 80pp; English
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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The probe,

methods and apparatus are useful

ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;

Novel human cDNA sequence #269

07-OCT-2004 ADQ63108;

(first

entry)

ADQ63108 standard;

CDNA; 1986

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RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 544
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                                                                                                                                                                                                                                        TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLys
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                                                                                                                                                                                                                      TATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACAAA
                                                                                                                                                                                                                                                                                       CATGGACGGGTTAATAATGTGTTTTGATCATTTTTTCAGATTGTGAATTTTTTGGCTGCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a nucleotide sequence of the invention.
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-2003;
09-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2004; 2004EP-00001196
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            GACTTAATCAAGGTGGCGATCAAAATCGGGATCCTCTACCGGAACAACCAGTTTAGCCAA
                                                                                                                                                    LeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLys
                                                                                                                                                                                                    ValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGlu
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                                                                                                      AsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGln
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GTCAGCTTCTATGAGGTGGAATACACCTTCGATAGGAACGTGCTCTCCAATCTCCTGCAT
                                                            AspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrVal
                                                                                                                                                                                       GCCAGCAAAACTGTGGCCAACATGTTGATTGATGACACCAGCAGCGAGATCTTTGATGAG
                                                                                                                                                                                                                                   GATGTTTTTAGTTCAAAGAGTCTTGCGCTTCAAGCCCAGAAGAATACTCTGAGCAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 269;
                                            GAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCATT
                                                                                                                                        Sugiyama T,
, Isono Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003JP-00102206.
2003JP-00131392.
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651.00
89.07%
62.30%
67.67%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2449pp; English.
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Matches:
Conservative:
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an enthod of detecting polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of poventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the

Claim 1; SEQ ID

NO 851; 1185pp; English.

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RESULT 18
ADC30769
ID ADC3
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                                                                                                                                                                                                                                                                                                   Tang TY, Zhang J
Zhou P, Ghosh M,
Haley-Vicente D,
New polynucleotide and polypeptide useful for diagnosing, preventing treating conditions such as neurodegenerative diseases, anemias, plat disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases of the conditions of 
                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                        WPI; 2003-371981/35.
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       The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide conding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that controlled in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule compressed in human cells or tissues. Also included are a spatially-conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-conditions to a nucleic acid molecule compressed in human cells or tissues. Also included are a spatially-conditions to a nucleic acid molecule expressed in human sense expression, a method of compression comprising at least spatially conditions of the plurality of single exon nucleic acid grobes cited above, an ORF-encoded peptide comprising at least specific contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids specifically to a peptide cited above, an organizated antibody that binds specifically to a peptide cited above, an organizate any appearance of a providing to measure gene expression, a method of providing the substitutions of a customer desiring to measure gene expression, a method of providing control of the substitutions of a single exon probe contends and appearatus are useful in gene customer desiring the substitutions of substitutions and characterising gross alterations in the grobes are used in i
smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Nete: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
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alternative splicing event; genomic alteration.
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                                Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telanglectasia; leukodystrophy; anxiety; pain; obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; atherosclerosis; hypertension; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficienncy; HIV; viral infection; neurogenesis; bacterial infection; parasitic infection; graft-versus-host disease; cell differentiation; cell proliferation; haematopoiesis; wound healing;
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28 - MAR - 2001;

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Spytek KA, Zhong ξ. KA, Vernet CA, Tchernev VT, Malyankar UM, Zerhusen BD, Patturajan M, Gusev VY, Kekuo M, Gangolli EA, Taupier RJ; Kekuda R, Gerlach VL; a R, Pena CEA;

2002-713508/77. DB; ABG97498.

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or Parkinson's disease. multiple

Claim 22; Page 139; 266pp; English.

The present invention relates to a new polypeptide (NOVX). The NOVX CC polypeptide, nucleic acid and antibody are useful in the manufacture of a comedicament for treating a syndrome associated with a human disease, competerably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or cc diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau cc syndrome, Alzheimer's disease, stroke, tuberous sclerosis, erebral cpalsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-cc telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, atherosclerosis, hypertension, cc scleroderma, haemophilia, disabetes, pancreatities, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and collecties that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, in gene therapy, in generation of antibodies that bind cangiogenesis, in gene therapy, in generation of antibodies that bind contended in the invention. The nucleic acids are further used as hybridisation content of the invention of the invention of the invention.

Sequence 619 BP; 97 **A** 219 Ç, 207 ດ 96 H. 0 ä

Homo sapiens

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                                         Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain; obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; atherosclerosis; hypertension; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parasitic infection; graft-versus-host disease; cell differentiation; cell proliferation; haematopoiesis; wound healing;
                                                                                                                                                                                                                                                                                                                      Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS78741 standard;
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Zhong M, Gangolli EA, ξ Zerhusen Vernet CA, 'Icucan nusen BD, Patturajan M, Tchernev VT, Malyankar UM, tturajan M, Gusev VY, Keku Kekuda R, Gerlach VL; Pena CEA;

WPI; 2002-713508/77. P-PSDB; ABG97497.

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or parkinson's disease. multiple

Claim 22; Page 139; 266pp; English.

CC syndrome, Althelmer's disease, stroke, tuberous sclerosis, crebral complete mental disease, stroke, tuberous sclerosis, crebral complete, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxiately apisectsaia, leukodystrophies, addiction, anxiety, depression, pain, cobesity, Crohn's disease, osteoporosis, inflammatory bowel disease, cinfertility, inflammatory bowel disease, atherosclerosis, hypertension, complete and the second disease, atherosclerosis, hypertension, complete and second disease, and complete and architis, immunodeficiencies, HTV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and complete hat modulate or inhibit e.g. neurogenesis, cell collections may also be used as targets for the identification of small complete hat modulate or inhibit e.g. neurogenesis, cell collections that bind complete and second disease, in generation, haematopolesis, wound healing and complete methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present nucleic acid sequence encodes a human NOVX contraction of the following preventive medicine, and contractions of the present nucleic acid sequence encodes a human NOVX contraction. medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture invention of a

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                                       Antiarteriosclerotic; cytostatic; HIV; antiallergic; antianaemic; antiarteriosclerotic; cardiant; vasotropic; neuroprotective; nootropic; SECP; anticonvulsant; antiparkinsonian; cerebroprotective; antiinflammatory; immunosuppressive; human secreted protein; cell proliferative disorder; arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; allergy; anaemia; asthma; cardiovascular disease; developmental disorder; ischaemic heart disease; congestive heart failure; neurological disorder; renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia; Parkinson's disease; epilepsy; stroke; knockin humanised animal; transgenic animal; gene therapy; gene; ds.
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                                                                                                                                                                                                       Alignment
                                                                                                                                                                                                                                                         The invention relates to an isolated human secreted protein (SECP)

CC polypeptide from 63 fully defined protein sequences given in the

CC specification. The polypeptide is useful for the diagnosing/treating of a

CC disease with decreased/overexpression of SECP. Examples of disorders

CC associated with abnormal expression of SECP include a cell proliferative

CC disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory

CC disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g.

CC congestive heart failure, ischaemic heart disease; developmental disorder

CC c.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g.

CC Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke.

CC file SECP polynucleotide and polypeptide are further useful for analysing

CC the proteome of a tissue or a cell type. The polynucleotide is useful for

CC creating knockin humanised animals (pigs) or transgenic animals (mice or

CC rats) to model human disease, and for somatic or germline gene therapy,

CC and further for generating hybridisation probes useful in mapping the

CC naturally occurring genomic sequence. This polynucleotide sequence

CC represents the DNA of a human secreted protein of the invention
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Tu DAM,
'n CH,
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09-NOV-2000;
16-NOV-2000;
21-NOV-2000;
08-DEC-2000;
18-DEC-2000;
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P-PSDB; AAO21665.
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Lia M, Thornton M, Elliott VS,
Hafalia AJA, Tang YT, Bandman
Thangavelu K, Lee S, Xu Y, Ya
Duggan BM, Sapperstein SK;
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GCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAGGCGCAGAAGAAGCTCCTGAGT
                                                AlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGly
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Ihornton M,
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region o (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3 a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human tumour-associated antigenic target (TAT) cDNA sequence #2473.
                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule and encoded polypeptide, i preventing or treating cell proliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour-associated antigenic target; TAT; cytostatic; gene therapy;
; cell proliferative disorder; gene; ss.
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Collength coding region of the above nucleotide sequence; or (c) a sequence comprising the above polypeptide fused to a heterologous polypeptide; (f) as isolated antibody that binds to the above polypeptide; (f) an isolated antibody that binds to the above polypeptide; (f) an isolated antibody that binds to the above polypeptide; (f) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (10) a composition of matter contained within the container; (11) methods of the composition of matter contained within the container; (12) methods of cinhibiting the growth of a cell that expresses the above protein, where the apove that express the above protein; (13) a method of cells that express the above protein; (13) a method of described above; (15) methods of diagnosing the protein of described above; (15) methods of diagnosing the protein above protein; and (17) a method of for treating or preventing a call proliferative or granic molecule to a cell that expresses the above protein or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or corganic molecule to a cell that expresses the protein described above. CC protein; and (17) a method of binding an antibody, oligopeptide or corganic molecule to a cell that expresses the protein described above. CC protein; and (17) a method of binding an antibody, oligopeptide or corganic molecule to a cell that expresses the protein described above. CC protein; and (17) a method of binding an antibody, oligopeptide or corganic molecule to a cell that expresses the protein described above. CC protein of a method of binding an antibody, oligopeptide or corganic molecule to a cell that expresses the protein of a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a 
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                                    Best Local Similarity:
                                               Percent Similarity:
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56.68%
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               HisGlyargValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu
                                                               TIGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCCACCTGACCGCCAAGTCC
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                                                                                           LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer
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CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC (a); (c) the complement of (a) or (b); (d) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC nucleotide sequences; (b) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC comprising the above polypeptide fused to a heterologous polypeptide
CC an isolated antibody that binds to the above polypeptide; (6)
CC an isolated antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC described above; (15) methods of diagnosing the presence of a tumour in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3626; 5504pp; English.
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RESULT 25
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ID ADQ84
XX
AC ADQ84
XX
DT 07-0C
XX
DE Human

ADQ84271 standard;

CDNA; 2186

В₽

ADQ84271; 07-OCT-2004

(first entry)

Human tumour-associated antigenic target (TAT) cDNA sequence #1085

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT CDNA sequence from the present invention.
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                              MetLeuAspGluGluAsnIle
                                                                                              TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLys
                                                                                                                             CACGGCCGATCAACCACGTGTTCGGCCACCTAGCCGACTGCGACTTCCTGGCTGCGCTC
                                                                                                                                                            HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu
                                                                                                                                                                                             CTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCC
                                                                                                                                                                                                                           LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer
                                                                                                                                                                                                                                                                                 ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu
                                                                                                                                                                                                                                                                                                                                                 AsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMet
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ATGCTGGACGAGGGCAGCCTC
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Percent Similarity:
Best Local Similarity:
                                                                                                                                CC target (TAXT) mucleic acid comprising: (a) any of 4622 nucleotide (c) the complement of (a) (b); (b) the full-length coding region of CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%; (c) (c); (d) the complement of (a) or (b); (d) a sequence that has 80%; (e) complement (c) and the has been coded by the full-length coding region of CC (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) (c) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-CC length coding region of the above nucleotide sequences; (c) a sequence comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody (b) an isolated oligopeptide; (f) a process cc for producing the antibody; (6) an isolated oligopeptide; (7) a process cc for producing the antibody; (6) an isolated antipody; (7) a process cc for producing the antibody; (8) an isolated antiponic target (TAT) antibody; (1) a manifecture comprising organic molecule that binds to the above polypeptide; (7) a process cc for producing the archively of the above (C) antibody; (10) a article of manifacture comprising a container and cc antibody; (1) a article of manifacture comprising a container and cc with a carrier; (11) an article of manifacture comprising a container and cc inhibiting the growth of a cell that expresses the above protein, where the growth of the above protein; (13) a method of determining the protein and carrier; (12) methods of container; (13) a method of determining the container and container. (14) a method of determining the container and container and container and container and container. (15) a method of container and container and container and container and containe
                                                                                              Alignment
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                                                                                                                                                                  medicament for the therapeutic treatment or diagnostic detection sell proliferative disorder or cancer. The present sequence represement TAT cDNA sequence from the present invention.
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) WU T D.
) ZHOU Y.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
 Ota T,
                                                                                                                                                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                  Human cDNA clone (5'-primer)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence)3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03165 to AAH13628 and AAH13632 to AAH18742 represent human cDNA sequences; ABB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent controlleds, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                            MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                                                                                                                    ATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAG
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                     LeuLeuAsnGluCys-ArgGluMetLeuHisGln 131
                                                                                                                                               TTTAATCAAGATGAGCTAGCATTGATGGNGAAATTTAAGAAGAAGTTCATCAGCTTGCT
                                                                                                                                                                    PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla
                                                                     ATGACCGTGGNCAGTTTCCAACAAGGGGGGTTATACCTTTGACCGGAATGTGTTATCCAAG
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Best Local Similarity: Percent Similarity:

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Mismatches: Indels: Matches: Conservative: Мо ::

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RESULT 27
ABK34943
  Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection; bacterial infection; fungal infection; diabetes; asthma autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.
                                                    and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
                                                                                                                                                                                      proteins. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroidits and diabetes) and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                          Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.
Sequence 1113
                                                                                                                                                                                                                                                                                                                            The invention relates to 592 polynucleotides which have been derived a variety of human tissue sources and which encode novel secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wong GG, C. Gulukota K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000; 2000US-0195582P
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                                    ABK34863-ABK35454 represent polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human LP237 secreted protein encoding
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                     28-SEP-2000; 2000US-0236088P
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The invention relates to human secreted polypeptides designated LP095, LP217, LP220, LP221, LP222, LP229, LP237 or LP238 and nucleic acid molecules encoding such polypeptides. Novel secreted proteins of the invention are used for treating diseases such as atherosclerosis, attention are used for treating diseases such as atherosclerosis, attention are used for treating diseases such as atherosclerosis, attention are used for treating diseases such as atherosclerosis, attention of the invention are used for encaptable arthritis, colorectal adenomas, severe combined immunodeficiency, ischaemia, carcinomas, haemolytic anaemia, reperfusion injury, neoplasms and cancer sepecially liver cancer. They are also used for wound healing. Polymucleotides of the invention can be used to generate transgenic animals or knock out animals, which in turn, are useful in the development and screening of therapeutically useful reagents for use in the treatment of diseases associated with LP polypeptide associated activity. They are also used in gene therapy. The present sequence is human LP237 secreted protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel proteins and polynucleotides of secreted proteins useful for treating various diseases e.g. rheumatoid arthritis, cancer, psoriasis, diabetic retinopathy, arteriosclerosis, ischemia or reperfusion injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 140-141; 145pp; English.
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BP; 305 A; 319 C; 312 G; 229
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US-10-627-571-2 (1-188) x AAD38699 (1-1165) 6.34e-50 527.00 77.22% 55.00% 54.78% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1165 99 40 39 1

26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr :::|||:::|| ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu GlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeuAspGlu CGCCACGTGTTTGATCACTTCTGTGACCCAGGTCTGCTCACGGCCCTCTATGGGCCT---PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGGAGAAGAAGCTACTGAGTAAGATGGCGGGT PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer AsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnProPhe ArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgVal LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer CGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC CGGGATGTGCTGCTAGAGTTGGTGGAACACCACCTCACGCCCAAGTCACATGGCCGCATC CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGGGTGCCATGACGGCACTTAGC CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCCCAGCGCGTGATCAAGGACCTG 165 145 125 185 45 168 468 408 105 348 65 25 585 528 85 288 228

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AC ABZ11
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AC ABZ1
AC ABZ11
A
                                 Percent Similarity:
Best Local Similarity:
                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                               CC nuclectide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynuclectides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or thung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC of the printed specification, but was obtained pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; blachemer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytoscatic; immunomodulator; noctropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemosstatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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T, Wang J, War
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Ma Y, Yamazaki V, Chen R,
, Wang D, Drmanac RT;
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                                                                                                                                                                                                          313 G; 232 T; 0 U; 0 Other;
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Mismatches:
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R, Wang Z,
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05-MAR-2002; 2002WO-US005095
20-AUG-2002; 2002US-00225251
                              WPI; 2004-238579/22
                                                                                                                                          (TANG/) TANG Y T. (XUEA/) XUE A. (DRMA/) DRMANAC R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic disorder
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in ageageing hiddressies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and
 Human cell cycle and proliferation
                                   24-APR-2001
                                                                   AAF59594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1175
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                                                                                                  AAF59594 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in assessing biodiversity. The present sequence represents a novel an arginine-rich protein cDNA.
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                                                                                                                                                                                              GlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeuAspGlu
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                                                                                                                                                                                                                                                                                                                   ArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGGGTGCCATGACGGCACTTAGC
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                                 (first entry)
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protein CCYPR-5 cDNA,

SEQ ID NO:59.

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LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr 45

PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer 25

TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGGAGAAGAAGCTACTGAGTAAGATGGCGGGT 171

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Query Match: DB:

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US-10-627-571-2 (1-188) x AAF59594 (1-1268)

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CC Sequences AAF59590-AAF59643 represent cDNAs encoding 54 human cell cycle CC and proliferation proteins (CCYPR), AAB60506. CCYPR and agonists CC of CCYPR are used to treat diseases or conditions associated with CC decreased expression of functional CCYPR, while CCYPR ancagonists are used to treat diseases or conditions associated with overexpression of functional CCYPR. Monoclonal or polyclonal antibodies to CCYPR may be comed in enzyme-linked immunosorbent assays (ELISA) or radioimmunoasays to cetect CCYPR. CCYPR itself may be used to detect compounds e.g., cc antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that condulate the activity of CCYPR. CCYPR mucleotides can be used in gene cethorapy in target cells with genetic abnormalities with respect to the therapy in target cells with genetic abnormalities with respect to the cexpression of CCYPR. Diseases which can be diagnosed, treated and cc associated with CCYPR. Diseases which can be diagnosed, treated and conclude immune, developmental and cell signalling disorders, and cell conclude immune, developmental and cell signaling disorders, and cell conclude induced by Actoria disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, infections caused by Actoria disorders of the menstrual cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1999;
08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112727/12.
P-PSDB; AAB60457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 171;
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caused by bacteria
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Baughn MR,
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Patterson
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                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                             New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental pharmaceutical; gene; ss.
                                                                                                                                             Claim 1;
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                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for throwing the contract of the contra
                              for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide sequences obtained from various cDNA libraries, as hybridization probes, as oligomers for PCR, for chromosome and smapping, in the recombinant production of protein, or in generating
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                                       New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACH76016
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                       surveying
                                                                                                                                               WPI; 2004-119264/12.
                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                 03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003194704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome derived single exon probe #9211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer 25
|||:::|||||:::|||||:::|||||:::|||
TCAGCTCAAAGAGCCTGGCAGCAGCAGAGAAGCAACTGAGTAAGATGGCGGGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheHisGlnValAspTyrThrPheAspArgAsnValLeuSer 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGGGTGCCATGACGGCACTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrValValSer 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGTGTCCAAGGAGTACACGCACAGCCCGGCCCCAGGCCCAGCGCGTGATCAAGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGGTGAGGTAGACTTCACCTTCGAGGCTGCTGTTCTGGCT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                       tissues.
                                                                                                                                                                                              Rank DR,
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324.00
78.95%
54.39%
33.68%
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Matches:
Conservative:
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Indels:
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Claim 15; SEQ ID NO 9211; 80pp; English

CC gene expression (comprising a plurality of single exon nucleic acid comprobes cited above, where each of the plurality of probes is separately cand addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of comprobe cited above, an ORF-encoded peptide comprising the single exon contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an cids of selling and/or licensing single exon probes or microarrays to contiguous amino acids specifically to a peptide cited above, an oRF-encoded peptide comprising at least 8 continuous and conservative amino acid substitutions), an cids of selling and/or licensing single exon probes or microarrays to contained the measure gene expression, a method of providing contained the contains a database having a plurality of records (each record including data on the expression, a method of providing contained the probes and apparatus are useful in gene content of the probes and apparatus are useful in gene content of the probes are used an including apparatus are useful in gene contained the probes are used in identifying and characterising gross content genomic alterations, in priming the synthesis of nucleic acids, cordinate exon probe of the invention. Note: The sequence data for this contained contained the probes are used in cludes their exon, in assessing shall exon probe of the invention. Note: The sequence data for this contained the probes are used as period at the austral data. hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that seqdata.uspto.gov/sequence.html?DocID=20030194704 The invention relates to a nucleic acid probe for measuring human expression, comprising any of the 27,400 fully defined nucleotide

Sequence 500 BP; 164 A; 71 Ç 107 G; 158 Ţ, 0 Ç, 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match: 4.25e-25 304.00 100.00% 100.00% 31.60% Length: Matches: Mismatches: Indels: Conservative: 000055

US-10-627-571-2 (1-188) x ACH76016 134 GlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSer ω CAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTTGATCATTTTTCA (1-500)

153

62

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AAH0472: RESULT 36 밁 S

AAH04721 standard; CDNA; 714 ВP

AAH04721;

26-JUN-2001 (first entry)

SXSXSXSXS CDNA clone (5'-primer) SEQ ID NO:1556.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; 88

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                                                                                                                                                                                                                                                                                                          Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T,
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
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                                                                                                 124
                                                                                                                                                                              104 ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn
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                                                                                                                                                      σ
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Sugiyama
                                                                            GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly
ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1556; 2537pp + Sequence Listing; English.
                                               GAGTGCCGCGACCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCCACGGC
                                                                                                                                                   GTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGCGTGCTGGCCGCCGGGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 A; 246
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292.00
81.18%
58.82%
30.35%
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203
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A, Nagai K,
                                                                                                                                                                                                                                                                                                    Gaps:
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Indels:
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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19
16
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                                                                                                 143
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RESULT 37
ADH18 ID
ADH18 XX
ANH18 XX
ANH18 XX
ANH18 XX
DT 26-JU
DT 26-JU
DX Human
XX
                       CC length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC oligonucleotide comprises a least 15 nucleotides; or (b) a combination

CC oligonucleotide comprising a sequence complementary to the

CC oncomplementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in the

CC particularly full-length cDNAs. The primers are useful for synthesising polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95993

CC present human amino acid sequences, and AAH13629 to AAH13627 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis of the abnormality of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota T, 1
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:18986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH18715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000EP-00116126
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, Sugiyama
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the full-length
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RESULT 38

ARK56622

ID ARK56

XX ARK56

XX ARK56

XX O6-NC

XX Human

XX Cytos

XX O9-AU

XX 17-JA

PR 11-MA

PR 11-MA

PR 11-MA

PR 11-JU

PR 26-JU

PR 26-JU
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
              31-JAN-2000;
04-FEB-2000;
04-FEB-2000;
02-MAR-2000;
16-MAR-2000;
11-MAR-2000;
11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
07-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
16-JUL-2000;
16-JUL-2000;
16-JUL-2000;
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                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                          immune/haematopoietic antigen encoding cDNA SEQ
                                                                                                                                                                                                                                                                                                                                                                    immune; haematopoietic; immune/haematopoietic antigen; cancer;
atic; gene therapy; vaccine; metastasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCCACGGC
2000US-017965P.
2000US-0184664P.
2000US-0184664P.
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2000US-0186350P.
2000US-0199076P.
2000US-0199076P.
2000US-0209467P.
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2000US-0215487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217489P.
2000US-0217496P.
2000US-0217496P.
2000US-0217496P.
2000US-0217496P.
2000US-022964P.
2000US-022964P.
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292.00
81.18%
58.82%
30.35%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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  14-AUG-2000
18-AUG-2000
18-AUG-2000
11-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
01-SEP-2000
01-SEP
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
2000US-0224519P.
2000US-022526P.
2000US-022526P.
2000US-022526P.
2000US-0225275P.
2000US-022575P.
2000US-023934P.
2000US-023934P.
2000US-0231243P.
2000US-0231243P.
2000US-0231414P.
2000US-0231414P.
2000US-0231243P.
2000US-0241786P.
2000US-0241786P.
2000US-02446178P.
2000US-0246474P.
2000US-0246477P.
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08-NOV-2000;
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01-DEC-2000

05-DEC-2000

05-DEC-2000

05-DEC-2000

06-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000
               amino acid sequences given in AAM82170 to AAM91921. (I) have cyrostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to product the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, and treat immune/haematopoietic_related diseases, especially cancers and cancer metastases of haematopoietic_derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic_derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                    Claim
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17-NOV-2000;
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7-NOV-2000;
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7-NOV-2000;
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                                                                                                                                                                                                                                                                                                                        to AAK64702 encode the human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1682;
                                                                                                                                                                                                                                                                                                                                                                                                          preventing,
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2000US-0246528P.
2000US-0246528P.
2000US-0246610P.
2000US-0246611P.
2000US-0246611P.
2000US-024920P.
2000US-024920P.
2000US-0249211P.
2000US-0
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2000US-0256719P
2000US-0251479P
2000US-0251856P
2000US-0251868P
2000US-0251868P
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2000US-0251990P.
2000US-0254097P.
2001US-0259678P.
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  the present
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                                                                                                                                                                                                                                                                                                                                                                                                        human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
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    invention.
  AAK54942 to
antigen genomic
AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                          antigen polypeptides, cancers and metastasis.
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Claim 1; SEQ

ID NO 14427;

71pp + Sequence Listing; English

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RESULT 39
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ID AAC10
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DB:
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                                                                        WPI;
                                                                                                                                                                                                                                            Human; 5' EST gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 441
                             diagnostic,
                                      New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                           21-FEB-2000; 2000EP-00200610
                                                                                                                                                                                                    EP1033401-A2
                                                                                                                                                                                                                                                                             Human
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                                                                                                                                                                                                                                                                                                                                            AAC10352 standard; cDNA; 340
                                                                                           Dumas Milne Edwards
                                                                                                                                     26-FEB-1999;
                                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                 (GEST ) GENSET
                                                                       2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                              329
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                                                                                                                                                                                                                                                                             secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer
                                                                                                                                                                                                                                                                                                                                                                                      TTGGT-GAAGTNGATTTCACT---
                                                                                                                                                                                                                                                                                                                                                                                                  PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCCCTGGCTAMCCGCTTTCGCCAGAARCTGCGGCAAGGTGCCATGAMGGCATTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCCAGCGCGTGATCAAGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAAGAAGCTACTGAGTAAGATGGCGGGT
                                                                                                                                                                                                                                                         EST;
                             forensic,
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 99
                                                                                                                                                                                                                                              chromosome mapping;
                                                                                                                                      99US-0122487P.
                                                                                                                                                                                                                                                                           protein 5'
                                                                                                                                                                                                                                                        expressed
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281.00
74.36%
51.28%
29.21%
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                            gene therapy and
                                                                                            Duclert
                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                            EST,
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                       tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 89
                                                                                            Giordano
                            chromosome mapping procedures
                                                                                                                                                                                                                                                        secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>, ,</del>
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60
27
24
                                       tag (5' EST) for
                                                                                                                                                                                                                                                         cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                      420
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and treating e.g. leukemia, inflammation and immune disorders.

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RESULT 40
AA192435/c
ID AA1924
XX AA1924
XX Human
XX Human;
KW Human;
KW Vaccin
KW Itissue
KW Nozoon
XX Homo s
XX Ho
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                      P-PSDB; AAO12504
                                                                                                     WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US004927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 12495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI92435;
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                                                                                                                                                                        YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTG
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                                                                                                                                                                        Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Gaps:
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing

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AAC10359
ID AAC10
XX AAC10
XX AAC10
XX AAC10
XX Human
XX Human
XX Homo
XX Gene
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiseis regulating activity, tissue growth factor activity, immunomodulatory activity and activity intibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                         Human; 5' EST;
gene therapy;
                Dumas Milne Edwards
                                                                                 26-FEB-1999;
                                                                                                                                                                              EP1033401-A2
                                                                                                                                                                                                                                                                                          Human secreted protein 5' EST,
                                                                                                                                                                                                                                                                                                                                                            AAC10359;
                                                                                                                                                                                                                                                                                                                                                                                           AAC10359 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                               21-FEB-2000; 2000EP-00200610
                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                            06-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 12495; 1399pp + Sequence Listing; English
                                                 (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 Ile 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 GATGAGCTGTACCGCGCCACCAGGAGTTCACGCGCAGCCGCAAGGAGGCCCAGAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                           chromosome
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                Duclert A,
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                                                                                                                                                                                                                                                                                          SEQ ID NO: 14434.
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                Giordano
                                                                                                                                                                                                                                                          secreted protein; cDNA isolation;
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RESULT 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome
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WPI; 2004-119264/12
                                                                                                                  (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                            03-APR-2002; 2002US-00029386
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                                                         Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s; se; gene expression; single exon probe; microarray;
splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derived single exon probe #11708.
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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
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Claim 15; SEQ ID NO 11708; 80pp; English

The invention relates to a nucleic acid probe for measuring human gene compression, comprising any of the 27,400 fully defined nucleotide companies in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences compared in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-compared to the plurality of probes is separately addressed be set of single exon nucleic acid probes for measuring human compared to the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon contiguous amino acids of any of the above-mentioned amino acid sequences (potionally with conservative amino acid substitutions), an including and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of records the above-mentioned amino acid substitutions) and contains and adatabase having a plurality of providing the storage medium which contains a database having a plurality of records (each record including data on the expression, a method of providing the storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying contain their problemants are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising gross alternations in the genomic locus that includes their exon, in assessing smaller genomic alternations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704 BP; 137 A; 128 C; 119 G; 159 T; 0 U; 0 Other;

Sequence 543

Percent Similarity: Best Local Similari Query Match: No.: Similarity: 2.4e-07 148.00 88.64% 54.55% 15.38% Length: Matches: Conservative: Mismatches: Indels: 543 24 15 0

US-10-627-571-2 (1-188) x ACH78513 (1-543)

ADP04796
ID ADP0
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AC ADP0 밁 밁 S 밁 S ADP04796 standard; cDNA; 1329 183 163 143 GlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyr 63 w LeuAspGluGlu 186 AGTCTGGATGGAGACTGTAGGCCCCAACCTCAAGAGGATTTGTGAAGGAATCAATAAGTTG AsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMet 182 GGGCGCATCAACCACGTCTTTAACCACTTTGCCGATGTGGAGTTCCTCCACCCTCTAT CTAGATGAGAAA 122 162 62

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                that are derived from the sea squirt clona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention describes the identification of these genes as useful for elucidation of the mechanism of development and hence for developing regeneration medicines and gene therapy techniques. Accordingly, they can be used in the research of various genetic diseases, as well as the analysis of cell proliferation, differentiation and reproduction. Furthermore, such compositions can be useful for environmental measurements and water surveys, particularly for sea water surveys, and also for the preparation of transformed sea squirt for improving edibility of sea squirt such as Halocynthia roretzi. This polynucleotide sequence is a sea squirt cDNA sequence that exhibits tissue specific expression during development,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel gene cluster which is specifically expressed in tissue or during developmental phase of sea squirt, useful for elucidation mechanism of development of tissue or organ of sea squirt.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1329
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                                                                                ValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeuIle
                                                                                                                                                   SerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyrArg
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LysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPhe-----Asn
                                                                                                                                                                                                                AsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLys
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Conservative:
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used
                                                                                                                                                                                             Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection.
                                                                                                                                                                 Disclosure; Page 549-550; 577pp; English
                                                                                                                                                                                                                                                          WPI; 2000-365347/31.
                                                                                                                                                                                                                                                                                                                                                 (HOFF/)
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CARUCCI D.
GARDNER M.
VENTER J C.
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protozoacide;
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 Tomato E-196 nucleotide sequence.
                                   09-MAR-2001
                                                                     AAA95803;
                                                                                                     AAA95803 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to identify drug resistance in P. falciparum. Sequencing of the
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                                                                                                                                                                                                                                                                                                           AAATTAACCACCGCAACGAATATGGCAAATAATAATAATATGCTCATGGAT------
                                                                                                                                                                                                                                                                                                                                          HisLeuThrAlaLysSerHisGlyArgValAsnAsn-----ValPheAspHisPheSer
                                                                                                                                                                                                                                                                                                                                                                            LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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104

TCTAAACTAGCTGAAAAAGAATCGGAGGTAAATAGTTTTGAGCGATATGTATCAACAATCC

GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 40

MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu TTGCTTACTACAGAGATCAAAGATAAAAGAGGTGAGTCTTCGGAGTAAC-----ACC 103

20

CAGGATCAGCTGATGAATTTGACTTCAGAGATCAAAGAACTTAAAGATGAAATCCAGAAA LeuaspGluLeuTyrargValThrargGluTyrThrGlnasnLysLysGlualaGluLys

60 163

223

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US-10-627-571-2 (1-188)

x AAA95803

(1-588)

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Percent Similarity:
Best Local Similari
                       Query
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                                                                                                                                                                                             Sequence 588 BP; 223 A;
                                                                                                                                                                                                                                           plant, this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid fragments from tobacco, corn, soybean proteins that are homologs to the MAR binding filam (MFPI), useful for development of novel phenotypes.
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MAR; NtMFP1-2; anchor protein;
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GACAATGTAAACAAGTTAAAGCAAGAG 562	AspGlyIleAsnLysMetLeuAspGlu 185	CTAATTGCTGATCTGAGAAAAAAAAAAACCTTAGGAGAATGGTGGATGCTGAGCTG 535	Phe	GGCACTGCCTTAAGTGAAGCAAGTAAAAATGAAGTG	137 LeuThrAlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGlu 156	TCAGATGCGAAGCTGTTGGGGGAACAAGAGAGAAGACACCTACACCAGCTTGAGGAACAACTT 439	SerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHis 136	ATTCAAAAGGAATACAGTGAGTTCAAGTCCAATTCTGATGAGAAGGTGGCT 379	LeuAlaMetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeu 118	AATGTGCAATTAAATTCTTTGCTCCTCGAGAGAGATGAATCTAAAAAAGAGCTTCATGCT 328	PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysValHisGln 98	AGAGAGAGAGAACTGGAGTTGAAATGTGTATCAGAAGACAACCTG 268	LysIleLysAsnLeuIleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGln 80

Search completed: July 28, 2005, 19:22:51 Job time : 563 secs

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Ygapop 10.0 , X
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
is the number of results predicted by chance to have a
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Copyright (c) 1993 - 2005 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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APPLICANT: Zhao, Haoran
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Modulators of Lymphocyte Activation and Migration
FILE REFERENCE: 02104-00130US
CURRENT APPLICATION NUMBER: US/10/491,545A
CURRENT APPLICATION NUMBER: US 60/327,212
PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR APPLICATION NUMBER: WO 60/327,212
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID MOS: 96
SOPTWARE: Patentin Ver. 2.1
SEQ ID MO 48
LENGTH: 1892
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US-10-491-545A-48
        Score:
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APPLICANT: Li, Congfen
APPLICANT: Liao, X. Char
APPLICANT: Masuda, Esteb
APPLICANT: Pardo, Jorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/10491545A Publication No. US20050130117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human TNF-induced protein GG2-1 mRNA,
OTHER INFORMATION: complete CDS
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9 US-10-437-963-64679

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Matches:
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Sequence 46, Appl
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Sequence 1784, Appl
Sequence 17, Appl
Sequence 1473, Ap
Sequence 1473, Ap
Sequence 24, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 2109, Appli
Sequence 14, Appl
Sequence 153, Ap
Sequence 53, Appl
Sequence 53, Appl
Sequence 178606,
Sequence 40, Appl
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Query Match:
DB:
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                                                                                               APPLICANT: KASID, Usha N.
APPLICANT: KUMAR, Deepak
APPLICANT: KUMAR, Deepak
APPLICANT: GOKHALE, Prafulla
APPLICANT: GOKHALE, Prafulla
APPLICANT: AHMAD, Imran
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 223316
CURRENT APPLICATION NUMBER: US/10/627,571
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR FILING DATE: 2001-01-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10627571 Publication No. US20040082771A1 GENERAL INFORMATION:
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NAME/KEY: misc_feature
                                                                                    LENGTH: 1915
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FILE REFERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIN version 3.2
SEQ ID NO 215
LENGTH: 1814
TYPE: DNA
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Best Local Similarity:
Query Match:
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US-10-755-889-215
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                                                                                                                                                                                                       Sequence 215, Applic
Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                               APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLEOTIDES AND TITLE OF INVENTION: PATHWAY
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Best Local Similarity:
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US-10-755-889-215
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               SOFTWARE: PatentIn version
SEQ ID NO 217
LENGTH: 2003
     TYPE: DNA
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sapiens

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APPLICANT: MOTTIS, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 497
LENGTH: 2034
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US-10-87-192-497
i Sequence 497, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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Sequence 39, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITILE OF INVENTION: POLYNUCLEOTIDES AND POLY
TITLE OF INVENTION: PATHWAY
FILLS REFERENCE: DO224 NP
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 2081
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; ORGANISM: Homo
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RESULT 7
US-10-087-192-496
'; Sequence 496, App
; Publication No. I
 APPLICANT: MOTTIS, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION UNMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FRETSEQ for Windows Version 4.0
SEQ ID NO 496
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Matches:
Conservative:
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US-10-07-065-98

Sequence 98, Application US/10097065

Publication No. US20030055236A1

GENERAL INFORMATION:

APPLICANT: MOOVE, Paul A. et al.

FILE REFERENCE: P2021P1

CURRENT APPLICATION NUMBER: US/10/097,065

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: ECT/US98/27059

PRIOR APPLICATION NUMBER: 60/070,923

PRIOR FILING DATE: 1997-12-18

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR APPLICATION NUMBER: 60/068,057

PRIOR APPLICATION NUMBER: 60/068,057

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PRIOR APPLICATION DATE: 1997-12-18
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; LENGTH: 58723
; TYPE: DNA
; ORGANISM: Homo s
US-10-087-192-496
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Best Local Similarity:
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                                                                                                                                                    SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
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LysMetLeuAspGluGluAsnIle 188
                                                                                    LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
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APPLICATION NUMBER: 60/068,006

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LENGTH: 1943
TYPE: DNA
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SOFTWARE: Patentin Ver. 2.0
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LOCATION: (1926)
OTHER INFORMATION: n &
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LOCATION: (161)
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OTHER INFORMATION:
NAME/KEY: SITE
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APPLICATION NUMBER: 60/068,054
FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/068,367
FILING DATE: 1997-12-19
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FILING DATE: 1997-12-18
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; OTHER INFORMATION: US-10-372-876-98
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PRIOR FILING DATE: 1999-06-17
PRIOR PELICATION NUMBER: PCT/US98/27059
PRIOR PELICATION NUMBER: 60/070,923
PRIOR APPLICATION NUMBER: 60/068,007
PRIOR PELING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,007
PRIOR FILING DATE: 1997-12-18
PRIOR PELICATION NUMBER: 60/068,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/068,006
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,369
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,367
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,169
PRIOR APPLICATION NUMBER: 60/068,169
PRIOR FILING DATE: 1997-12-19
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                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 110 Human Secreted Proteins FILE REFERENCE: P2021P1 CURRENT APPLICATION NUMBER: US/10/372,876 CURRENT FILING DATE: 2003-02-26
                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: SITE
LOCATION: (161)
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                                     FEATURE:
NAME/KEY: SITE
LOCATION: (1934)
                                                                                                   OTHER INFORMATION:
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ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 2059

SOPTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 494
LENGTH: 2087

TYPE: DNA
ORGANISM: Mus musculus
US-10-087-192-494
                                                                                                                                                                                                                                RESULT 10
US-10-087-192-494
US-10-087-192-494
; Sequence 494, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                APPLICANT: Morris, David W. APPLICANT: Engelhard, Eric
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                               APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
FITLE OF INVENTION: CONCER
FITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 99/747,377
PRIOR APPLICATION NUMBER: US 99/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-02
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US-10-087-192-493
; Sequence 493, Application US/10
; Publication No. US20020182586A1
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                         NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 493
LENGTH: 62231
                                                                                                                                                                                                                                           GENERAL INFORMATION:
              TYPE: DNA
ORGANISM: Mus musculus
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Sequence 22914, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION UNUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288
SOFTWARE: AANOMAX Sequence Listing Engine vers. 1.1
SEQ ID NO 22914
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; NAME/KEY: misc_feature

; LOCATION: (1)...(62231)

; OTHER INFORMATION: n = A,T,

US-10-087-192-493
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Best Local Similarity:
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US-10-029-386-22914
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 US-10-029-386-25411

Sequence 25411, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: HANZEL, DAVID K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20
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ORGANISM: HOMO E
FEATURE:
OTHER INFORMATIC
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NN: EXPRESSED IN HELA, SIGNAL = 2.3

NN: EXPRESSED IN HEAIN, SIGNAL = 1.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

NN: EXPRESSED IN HEART, SIGNAL = 2.6

NN: EXPRESSED IN HEART, SIGNAL = 2.6

NN: EXPRESSED IN HEART, SIGNAL = 2.6

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

NN: EXPRESSED IN HEART, SIGNAL = 2.6

NN: EXPRESSED IN HEATT, SIGNAL = 2.6

NN: SWISSPROT HIT: P31390, EVALUE 2.60e-01

NN: NT HIT: g17657123, EVALUE 0.00e+00
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TYPE: DNA
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEACTURE:
; OFHER INFORMATION: MAP TO ACO12678.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.51
; OTHER INFORMATION: SWISSPROT HIT: Q61766, EVALUE 1.10e-01
; OTHER INFORMATION: NT HIT: AF120995.1, EVALUE 1.30e-01
; OTHER INFORMATION: EST_HUMAN HIT: BF744133.1, EVALUE 2.00e-59
US-10-029-386-25411
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                                                                                                              Sequence 43, Application US/10094466 Publication No. US20030203363A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence |
SEQ ID NO 25411
LENGTH: 527
                                          APPLICANT: Spytck et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS,
TITLE OF INVENTION: AND METHODS OF USING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-290D
CURRENT APPLICATION NUMBER: US/10/094,466
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,281
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; TYPE: DNA.
; ORGANIEM: Homo Bapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(566)
US-10-094-466-43
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Best Local Similarity:
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Pred. No.:
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PRIOR
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OR APPLICATION NUMBER: 60/288,148
OR FILING DATE: 2001-05-02
OR APPLICATION NUMBER: 60/274,849
OR APPLICATION NUMBER: 60/275,235
OR FILING DATE: 2001-03-02
OR APPLICATION NUMBER: 60/275,235
OR FILING DATE: 2001-12-04
OR APPLICATION NUMBER: 60/275,579
OR APPLICATION NUMBER: 60/275,579
OR APPLICATION NUMBER: 60/335,302
OR APPLICATION NUMBER: 60/335,302
OR APPLICATION NUMBER: 60/375,601
OR APPLICATION NUMBER: 60/275,601
OR APPLICATION NUMBER: 60/275,000
OR APPLICATION NUMBER: 60/276,000
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OR APPLICATION NUMBER: 60/276,000
OR APPLICATION NUMBER: 60/277,338
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RESULT 15
US-10-094-466-41
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CURRENT APPLICATION NUMBER: US/10/094,466

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/274,281

PRIOR FILING DATE: 2001-03-08

PRIOR PILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/274,849

PRIOR APPLICATION NUMBER: 60/274,849

PRIOR FILING DATE: 2001-03-09

PRIOR FILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/275,235

PRIOR APPLICATION NUMBER: 60/275,235

PRIOR APPLICATION NUMBER: 60/338,375

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: 60/338,375

PRIOR FILING DATE: 2001-12-04

PRIOR FILING DATE: 2001-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior Application data removed -
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PAIN 2.1
SEQ ID NO 41
LENGTH: 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/335,302
PRIOR FILING DATE: 2001-10-31
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Spytek et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS,
TITLE OF INVENTION: AND METHODS OF USING
TITLE OF INVENTION: THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/276,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo FEATURE:
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LOCATION: (26)..(584)
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APPLICATION NUMBER: 60/335,302
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                                                                                                                                             AGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGATGACACCAGCAGTGAGGTGGTGAGTGCTG
                                                                                       LysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeu
   GATGAGCTGTACCGCGCCACCAGGGAGTTCACGCGCAGCCGCAAGGAGGCCCAGAAGATG
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                               AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
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APPLICANT: DUGGAN, Brendan M.
APPLICANT: DUGGAN, Brendan M.
TITLE OF INVENTION: SECRETED PROTEINS
FILE REFERENCE: PI-02.87 USN
CURRENT APPLICATION NUMBER: US/10/416,314
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/247,505
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/249,642
PRIOR APPLICATION NUMBER: US 60/249,824
PRIOR APPLICATION NUMBER: US 60/249,824
PRIOR APPLICATION NUMBER: US 60/249,824
PRIOR APPLICATION NUMBER: US 60/252,824
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; Publication No. US200
; GENERAL INFORMATION:
; APPLICANT: YUE, Henr
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CHAMLA, Narinder K.
SANJANWALA, Madhusudan M.
THORNTON, Michael B.
ELLIOTT, Vicki S.
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WARREN, Bridget A.
HONCHELL, Cynthia D.
LU, Dyung Aina M.
THANGAVELU, Kavitha
LEE, Sally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACGGCCCCGCCGAGCCCTACCGCTCCCACCTGCGCAGGATCTGCGAGGGCCTGGGCCGG
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HAFALIA, Apri
TANG, Y. Tom
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                                                                                                                                                                                                                               TRAN, Bao
ISON, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LU, Yan
GIETZEN, Kimberly J.
BURFORD, Neil
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lo. US20040082508A1
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Query DB:

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; PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/254,305
PRIOR ETLING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/256,448
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PERL PROGram
SEQ ID NO 70
SEQ ID NO 70
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Best Local Similarity:
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DB:
                                                                                      US-09-816-828-5
                                                                                                     RESULT 17
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Sequence 5, Application US/09816828
Patent NO. US20020150898A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2108
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incy
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                                                                                                                                        ATGCTGGACGAGGGCAGCCTC
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; TYPE: DNA
; ORGANISM: Homo sapi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)..(7
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TITLE OF INVENTION: No. US20020150898A1el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIPZE
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
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     TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLys
                                                     HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu
                                                                                                   CTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCC
                                                                                                                        LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer
                                                                                                                                                                   ACGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGCGTGCTGGCCGTCGGC
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Wang, Jian-Rui
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APPLICANT: Tan, Yejun
APPLICANT: Dai, Hongyue
APPLICANT: Dai, Hongyue
TITLE OF INVENTION: Methods For Determining Whether An
TITLE OF INVENTION: Possesses A Defined Biological Act
FILE REFERENCE: ROSA122057
CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR APPLICATION NUMBER: US 60/474,413
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 3683
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US-10-764-420-2116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: 80
COTHER INFORMATION: n = A,T,C
US-10-764-420-2116
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SEQ ID NO 2116
LENGTH: 1389
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APPLICANT: Lum, Pek Yee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
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  447
                                                    387
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                                                                                                                                                                                                                                                             147 GCTTCCAAGGCCATGGTGGCTGTGTTGTGGACAATACCAGCAGTGAGGTCTTGGATGAA
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              GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly
                                                               GAGTGCAGGGACCTGTTGCACCAGGCTATTGGCCCGCACCTCACTGCCAAGTCCCACGGC
                                                                                                    AATGAGCTGGCCCAGCTGCAGCGGTTCCGGGGCGTCCGCCAACCTGGCCATGACAGCC
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                                                                                                                       AspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrVal 103
                                                                                                                                                                                                         CTGTACCAGGCCACGAAGGAGTTCACGCGCACGCGGAAGGAGGCACAGAGGGTAGTGAAG
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GENERAL INFORMATION:

APPLICANT: Wong, Gordon G.

APPLICANT: Wong, Gordon G.

APPLICANT: Fechtel, Kim

APPLICANT: Fechtel, Kim

APPLICANT: Agostino, Michael J.

APPLICANT: Agostino, Michael J.

APPLICANT: Resnick, Richard J.

APPLICANT: Gulukota, Kamalakar

APPLICANT: Graham, James R.

APPLICANT: Graham, 
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PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
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                                                                                                                                         LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICAGCICAAAGAGCCIGGCACIGCAAGCAGAAGAAGAAGCIACIGAGIAAGAIGGCGGGT 131
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                                                                                                                                                                                                                                                                                         IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                                                                                                                                                                        CGTGTGTCCAAGGAGTACACGCACAGCCGGGCCCCAGGCCCAGCGCGTGATCAAGGACCTG
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                                                                                                      ĊŢĠĠĊĊĊŢĠĠĊŢĄĊĊĠĠĊŢŢŢĊĠĊĊĄĠĄĄĠĊŢĠĊĊĄŢĠĄĊĠĠĊĄĊŢŢĄĠĊ
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; LOCATION: (100)..(651)
; FEATURE:
; HAME/KEY: sig_peptide
; LOCATION: (100)..(180)
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TITLE OF INVENTION: NOVEL SECRETED PROTEINS.
FILE REFERENCE: X13020
CURRENT APPLICATION NUMBER: US/10/363,374
CURRENT FILING DATE: 203-02-27
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.2
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/10363374
Publication No. US20050048483A1
GENERAL INFORMATION:
APPLICANT: Su, Exic
APPLICANT: Wang, He
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ORGANISM: Homo
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                         PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys 125
                                                                                                                    ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                    LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer
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                                                                                                                                               IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                               CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCCAGCGCGTGATCAAGGACCTG
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SEQ ID NO 537
LENGTH: 1175
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APPLICANT: Xue, Aidong J.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20040053250A1el Arginine-rich
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803 1CNCP
CURRENT APPLICATION NUMBER: US/10/302,172
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TYPE: DNA
ORGANISM: Homo
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PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
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NUMBER OF SEQ ID NOS: 950
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NAME/KEY: CDS
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106 PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys
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                                                                                                                                                                                                                 46 ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
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                                                                                                              ATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG
                                       CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGGGTGCCATGACGGCACTTAGC
                                                                       LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID
US-10-959-539-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/145,075; 60/153,129; 60/164,647
PRIOR APPLICATION NUMBER: 60/145,075; 60/153,129; 60/164,647
PRIOR FILING DATE: 1999-07-21; 1999-09-08; 1999-11-10
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PERL Program
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US/10/031,915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: HILLMAN, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHAH, PUTVI
TITLE OF INVENTION: CELL CYCLE AND PROLIFERATION PROTEINS
FILE REFERENCE: PF-0722 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1268
                                                                            172 CGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
                                                                                                                                                   112 TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAAGAAGCTACTGAGTAAGATGGCGGGT 171
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                                       46
                                                                                                        26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
                                                                                                                                                                     6 PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer
                               ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCAGGCCCAGCGCGTGATCAAGGACCTG
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LU, Dyung Aina M.
BAUGHN, Mariah R.
PATTERSON, Chandra
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BANDMAN, Olga
AZIMZAI, Yalda
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YUE, Henry
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77.22%
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Matches:
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US-09-796-692-3207
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                 Alignment Scores: Pred. No.:
                                                                        ; ORGANISM: Homo US-09-796-692-3207
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILLING DATE: 2000-05-22
PRIOR PPLICATION NUMBER: 60/218,950
PRIOR FILLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 3207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT PILLING DATE: 2001-03-01
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
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                                                                                                                                                                                      PRIOR FILING DATE: 2000-08
NUMBER OF SEQ ID NOS: 9597
                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-08-04 PRIOR APPLICATION NUMBER: 60/223,378
                                                                                                                  TYPE:
                                                                                                                                 LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 CGCCACGTGTTTGATCACTTCTGTGACCCAGGTCTGCTCACGGCCCTCTATGGGCCT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 ATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG
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Length:
Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-040-862-3207
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CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR PPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
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                       SOFTWARE: Fast
SEQ ID NO 3207
LENGTH: 287
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APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corpositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaiger,
APPLICANT: Algate
                                                                                             NUMBER OF SEQ ID
                                                                                                              PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                                       APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
FILING DATE: 2000-08-03
APPLICATION NUMBER: US 60/223,416
FILING DATE: 2000-08-04
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APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
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FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
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US20030078396A1
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                                                                     Version 3.0
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Indels:
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                                                       FILE REPERENCE: 01458-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/207
PRIOR APPLICATION NUMBER: US 60/208,950
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                       APPLICATION NUMBER: US 60/222,903 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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Prior Application data removed -
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Clapper, Jonathan
Wang, Aijun
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Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Matches:
Conservative:
Mismatches:
Indels:
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See File Wrapper or PALM
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Therapy

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APPLICANT: Galger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Det
TITLE OF INVENTION: Compositions and Methods for the Det
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TITLE OF INVENTION: Compositions and Methods for the Det
TITLE OF INVENTION INDEER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/220,993
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-03
PRIOR PILING DATE: 2000-05-04
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Best Local Similarity:
Query Match:
DB:
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US-10-154-884B-3207
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; ORGANISM: Homo sapiens
US-10-057-475B-3207
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
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APPLICANT: COTICA COMPOSATION AND Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-013520US

CURRENT PILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: US/10/764,324

CURRENT FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US/10/40,862

PRIOR APPLICATION NUMBER: US/10/40,862

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,399

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR APPLICATION NUMBER: US 60/200,099

PRIOR APPLICATION NUMBER: US 60/206,201

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04
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Query Match:
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NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3207, Application US/10764324 Publication No. US20040175739A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Algate, Paul APPLICANT: Mannion, Jane APPLICANT: Retter, Marc
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Matches:
Conservative:
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CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PILLING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/202,084
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; ORGANISM: Homo sapiens
US-10-764-324-3207
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NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2801, Application US/09796692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
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RESULT 29
US-10-040-862-2801/c
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Best Local Similarity:
Query Match:
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR HILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/206,201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions and Methods for the Detection, TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013520US
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PRIOR FILING DATE: 2000-08-04
PRIOR PPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
NUMBER OF SECTIONS: 9597
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Mannion, Jane
Retter, Marc
Corporation
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and Therapy

DATE:

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APPLICANT: Mannion, Jane
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Ordonez, Nadia
APPLICANT: Carteer, Lauren
APPLICANT: Cortonez, Nadia
APPLICANT: Compositions and Methods for the Detection, Dia-
TITLE OF INVENTION: Compositions and Methods for the Detection, Dia-
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
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Query Match:
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PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR PILING DATE: 2000-08-07
PRIOR PILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
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LENGTH: 287
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathar
APPLICANT: Wang, Aijun
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SOFTWARE: FastSEQ for Windows Version
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Indels:
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US-10-154-884B-2801/c
Sequence 2801, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
Remaining Prior Application data removed - Sei
NUMBER OF SEQ ID NOS: 10979
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Best Local Similari
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LENGTH: 287
               TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013521US CURRENT APPLICATION NUMBER: US/10/154,884B CURRENT FILING DATE: 2002-05-23 PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR PILING DATE: 2000-03-01 PRIOR PILING DATE: 2000-03-17 PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                           APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
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APPLICATION NUMBER: US 60/200,545
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APPLICANT: Galger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jame
APPLICANT: Mannion, Jame
APPLICANT: Metter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Dia
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/10/40,862
PRIOR APPLICATION NUMBER: US/0/186,126
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NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2801
LENGTH: 287
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                                                                                                                                                                                                                                                                                  Sequence 2801, Application US/10764324 Publication No. US20040175739A1
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OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: US 60/200,999
OR FILING DATE: 2000-05-01
OR APPLICATION NUMBER: US 60/202,084
OR FILING DATE: 2000-05-04
OR APPLICATION NUMBER: US 60/206,201
OR APPLICATION NUMBER: US 60/206,201
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APPLICATION NUMBER: US 60/218,950
         APPLICATION NUMBER: US 60/186,126 FILING DATE: 2000-03-01
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Manmion, Jane
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
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Percent Similarity:
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TRNGTH: 287
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
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TYPE: DNA
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FILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,999
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APPLICATION NUMBER: US 60/202,084
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                                                                                                                         US-10-040-862-5724
                                                                                                                                             RESULT
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5724
LENGTH: 288
Type: No.
Sequence 5724, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
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LCCATION: (58)
OTHER INFORMATION: I
NAME/KEY: unsure
LCCATION: (59)
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ORGANISM: Homo :
FEATURE:
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DR FILING DATE: 2000-04-28
DR PPLICATION NUMBER: 60/200,779
DR APPLICATION NUMBER: 60/200,999
DR FILING DATE: 2000-05-01
DR APPLICATION NUMBER: 60/202,084
DR APPLICATION NUMBER: 60/202,084
DR FILING DATE: 2000-05-04
DR APPLICATION NUMBER: 60/206,201
DR APPLICATION NUMBER: 60/216,201
DR FILING DATE: 2000-05-02
DR APPLICATION NUMBER: 60/218,950
DR FILING DATE: 2000-05-02
DR FILING DATE: 2000-05-07-14
DR PERICANTION NUMBER: 60/218,950
DR FILING DATE: 2000-07-14
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FILING DATE: 2000-08-03
APPLICATION NUMBER: 60/223,416
FILING DATE: 2000-08-04
APPLICATION NUMBER: 60/223,378
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and There
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT FILING DATE: 0301-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/206,201
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; NAME/KEY: unsure
; LOCATION: (59)
; OTHER INFORMATION: r
US-10-040-862-5724
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: n=A,7
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PRIOR FILLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILLING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR APPLICATION NUMBER: US 60/223,378
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183
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; FEATURE:
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US-10-057-475B-5724
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US-10-057-475B-5724
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR PPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR PPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5724
LENGTH: 288
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CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
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APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
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Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Clapper, Jonathan David
Wang, Aijun
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US-10-627-571-2 (1-188) x US-10-154-884B-5724 (1-288)
                                                                Query Match:
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5724
LENGTH: 288
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(288)
OTHER INFORMATION: n =
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OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: US 60/200,999
OR APPLICATION NUMBER: US 60/200,999
OR FILING DATE: 2000-05-01
OR APPLICATION NUMBER: US 60/202,084
OR FILING DATE: 2000-05-04
OR FILING DATE: 2000-05-20
OR APPLICATION NUMBER: US 60/218,950
OR APPLICATION NUMBER: US 60/218,950
OR APPLICATION NUMBER: US 60/222,903
OR FILING DATE: 2000-07-14
OR APPLICATION NUMBER: US 60/222,903
OR FILING DATE: 2000-08-03
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Retter, Marc W.
Corixa Corporation
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                    Alignment Scores:
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US-10-764-324-5724
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SEQ ID NO 5724
LENGTH: 288
                                                                              NAME/KEY: unsure
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
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                                                                                                                                               FEATURE:
NAME/KEY: unsure
LOCATION: (58)
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
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PRIOR FILING DATE: 2001-11-06
                                                                     LOCATION: (59)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rAspCysGluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPhe 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACCGGAATGTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTTGATCATTTTTTC
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     288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 35521, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OF; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/218,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
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US-09-918-995-35521
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; ORGANISM: Homo sapiens
US-09-918-995-35521
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Best Local Similarity:
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                  66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
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LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
                                                                                                                                                                             TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAAAGAAGCTACTGAGTAAGATGGCGGGT 136
                                                                                                                                                                                                  IleLeuTyrArgAsnAsnGlnPheAsnGlnAspGluLeuAlaLeuMetGluLys-PheLy
                                                   CGTGTGTCCAAGGAGTACACGCACAGCCCGGCCCAGGCCCAGCGCGTGATCAAGGACCTG
                                                                     ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                                                  CGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
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Matches:
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OTHER INFORMATION: M.
OTHER INFORMATION: E.
OTHER INFORMATION: M.
                                                                          RESULT 40
US-10-972-079-232
, Sequence 232, Application US/10972079
, Publication No. US20050153317A1
, PRNERAL INFORMATION:
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US-10-029-386-9211
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NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers.

SEQ ID NO 9211

LENGTH: 500

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9211, Application US/10029386 Publication No. US20030194704A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                 APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE; ABOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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                                                                                                                                                                                                                                                                                                                                                                                      134 GlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSer 153
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                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                               AspCysGluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPheLysProHisLeuGln 173
                                                                                                                                                                                                                   AAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATA 167
           DeNISE, Sue K.
ROSENFELD, David
KERR, Richard
BATES, Stephen
                                                                                                                                                                                                                                                  LysLeuCysAspGlyIleAsnLysMetLeuAspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                        GATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTTTAAACCCCCACTTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCAAAGTGGCCATCAAGGTGGCTGCTGCACCGCAATGGCTCCTTTTGGCCCCCAGTGAG 316
                                                                                                                                                                                                                                                                                                                                                                 CAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTTGATCATTTTTCA
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Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N: MAP TO AC035144.2

N: EXPRESSED IN HELA, SIGNAL = 2.3

N: EXPRESSED IN BRAIN, SIGNAL = 1.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 2.4

N: NT HIT: 9114725421, EVALUE 0.00e+00

N: EST_HUMAN HIT: BG178783.1, EVALUE 0.00e+00
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304.00
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31.60%
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Conservative:
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US-10-191-803-330/c
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                                Alignment Scores:
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Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Chicken
US-10-972-079-232
                 Pred. No.:
                                                                       US-10-191-803-330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                           SOFTWARE: Patentin Ver. SEQ ID NO 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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SEQ ID NO 232
                                                                                          OTHER INFORMATION:
                                                                                                                                              TYPE: DNA
                                                                                                                                                             ENGTH:
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APPLICANT: JOHNSON, Kory
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR APPLICATION NUMBER: US 60/355.
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 330, Application US/10191803
Publication No. US20040014040A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEE TITLE OF INVENTION: LIVESTOCK FILE REFERENCE; MMIII10-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 96631
                                                                                                                                           ORGANISM: Rattus norvegicus FEATURE:
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Best Local Similarity:
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                                                                                                                                                        Sequence 4917, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11708
LENGTH: 543
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
   APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE: TOTAL TOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 GlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyr
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Det
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/180,479
PRIOR FILING DATE: 2000-03-01
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Sequence 4917, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:

Detection,

Diagnosis and

Therapy

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PRIOR APPLICATION UNDER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 4917
LENGTH: 538
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Best Local Similarity:
Query Match:
US-10-040-862-4917/c
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US-09-796-692-4917
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,779
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PRIOR APPLICATION NUMBER: 60/200,779
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PRIOR APPLICATION NUMBER: 60/200,999
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                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: unsure
LOCATION: (77)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/218,950
FILING DATE: 2000-07-14
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FILING DATE: 2000-05-04
APPLICATION NUMBER: 60/206,201
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                                                          169 LysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeuAspGluGluAsnIle 188
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Matches:
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APPLICATION NUMBER: US 60/200,303 FILING DATE: 2000-04-28

APPLICATION NUMBER: US 60/200,545 FILING DATE: 2000-04-27

APPLICATION NUMBER: US 60/200,779

FILING DATE: 2000-04-28

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RESULT 45

US-10-057-475B-4917/c

Sequence 4917, Application US/10057475B

PUDIICATION 10. US20040002068A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Clapper, Jonathan David

APPLICANT: Wang, Aijun
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Best Local Similarity:
Query Match:
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; LOCATION: (77)
; OTHER INFORMATION: n=A,T,C
US-10-040-862-4917
APPLICATION Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4917
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/223,378
FILING DATE: 2000-08-07
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APPLICATION NUMBER: US 60/218,950
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FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 AAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATA 479
                                                                                                                                                                                                                                     Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Search completed: July 28, 2005, 19:36:11 Job time: 671 secs
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SEQ ID NO 4917
LENGTH: 538
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 10979
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APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
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APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
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                                                                    538 AAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGA
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=Xlh
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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MetAlaThrAspValPheAsn 	US-10-627-571-2 (1-188) x CN305329 (1-737)	Alignment Scores: Pred. No.: 954.00 Percent Similarity: 99.47\$ Conservative: Query Match: 99.17\$ DB: Alignment Scores: 6.73e-105 Length: 737 Matches: 187 Conservative: Onservative: Onservative:	Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 737	wski, J and Stanton, L W. criptome characterization elu ol human ES cell growth and d Biotechnol. 22 (6), 707-716 (ct: Brandenberger R cerative Medicine Corporation Constitution Drive, Menlo Park	Eukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 737) Brandenberger, Wei, H., Zhang, S., Lei, S., Mei, Y., Chang, S., Chang,	RESULT 1 CN305329 CN305329 CN305329 TOCUS DEFINITION 17000600027114 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence. ACCESSION CN305329 VERSION CN305329.1 GI:47321743 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens	772 80.2 582 5 BP261675 BP261675 770.5 80.1 680 4 BJ068640 BJ068640 757 78.7 517 6 CD372026 CD372026	83 807 83.9 622 6 CB553311 CCB553311 MMSP0007 84 801 83.3 588 7 CR787140 CR787140 DKPZP469G 85 799.5 83.1 771 6 CD521069 CD521069 AGENCOURT 86 799.5 83.1 829 7 CK804285 CK804285 AGENCOURT 87 799 83.1 674 2 BB667314 BB781663 CD2104381 BP781663 CD2104381 BD245938 BD24598 BD24598 BD24598 BD24598 BD2458 BD245
	/organism="Homo sapiens" /mol_type="mRNA"	Clone distribution: MGC Clone distribution can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM389 row: j column: 24 High quality sequence stop: 635. FEATURES Source 1780	VERSION CB990165.1 GI:30284685 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 780) AUTHORS NHI-MGC http://mgc.nci.nih.gov/. TITLE JOURNAL Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Stefan Hansson cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN) CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) NAS Semiencian by: Agenceurt Risagience Cornoration	Db 647 AAAATGTTGGATGAAGAAAACATA 670 RESULT 2 CB990165 CB990165 CB990165 CB990165 CB990165 CB990165 T80 bp mRNA linear EST 01-MAY-2003 DEFINITION AGENCOURT 13902271 NIH MGC 147 Homo sapiens cDNA clone IMAGE 13037855 5', mRNA sequence. ACCESSION CB990165	181 LYSMETLEUNBPGINGINASTILE 188	Qy 121 LeuLeuAsnGluCysArgGluWetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys 140	OY 1	107 ATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAGAAGATCTTG 21 GlyLysMetValSerIJsSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal

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Percent Similarity:
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IMAGE: 30528465 5', mRNA sequence
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sapiens (human)
sapiens
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/clone="Organ: placent; Vector: pBluescriptR; Site 1:
/note="Organ: placent; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
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DEFINITION

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SOURCE ORGANISM

101 MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg

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KEYWORDS VERSION ACCESSION

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COMMENT
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Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 2089
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1. (bases 1 to 806)
NIH-MGC hettp://mgc.nci.nih.gov/
National Institutes of Health, !
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High quality sequence stop: 648.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
a NIH_MGC library."
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/tissue_type="Human Placenta"
/lab_host="DH10B TonA"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 813)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone lib="NIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pcMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/db_xref="teaxon:9606"
/clone="IMAGE:5175702"
/lab_host="DH10B"
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AGENCOURT 15178772 NIH MGC 192 Homo sapiens
IMAGE:30512832 5', mRNA sequence.
CF272384
                                                                                                                                                                          Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 2089
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                    cDNA Library Preparation: Agencourt CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov column: 01
                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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Mammalia; Eutheria;
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e: NDAM573 row: m column: 01
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Location/Qualifiers
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                  SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
                                                                                            LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys 140
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TCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Brain glioblastoma"
/tissue type="Brain glioblastoma"
/lab_hoff="Wellon (T1 phage-resistant)"
/clone lib="MIH MGC 192"
/clone Tib="MIH MGC 192"
/clone Tib="Wellon: pExpress; Site_1: Smal; Site_2: NotI; The library was constructed by reverse transcription of 1 ug mRNA using the oligo dT primer GCGCCGCC(T) 20 and an RNaseH + MMLV reverse transcriptase. Second strand synthesis was carried out by standard methods. The cDNA was size selected by agarose gel for > 1.2 kb, digested with Not I and directionally cloned into the vector Express-1 at the Small/NotI sites. DNA from the primary library was used for in vitro transcription from the T7 promother to produce biotinylated RNA transcripts. These biotinylated transcripts, along with blocking oligos to the poly-A, multiple cloning site and primer regions, were hybridized with single stranded circles produced by phagmeid production from the primary library to a Cot value of 10-20. Strepavidin/phenol extraction was utilized stransformed back into E. coli resulting in the normalized library. Average insert size 2.0 kb. 3
linker/adaptor sequence GCGCCCCC(T) 20. This libary was
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                     Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rbrandenberger@geron.com
Insert Length: 712 Std Error: 0.00
Location/Qualifiers
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LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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                                                     CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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RESULT 7
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                         Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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AGENCOURT 14353034 NIH MGC 191 Homo
IMAGE:30413002 5', mRNA sequence.
CD521721
CD521721.1 GI:31453439
EST.
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High quality sequence stop: 603.
Location/Qualifiers
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   /clone="IMAGE:30413002"
/tissue_type="Pooled"
/lab_host="PH10B (TI phage-resistant)"
/lab_host="PH10B (TI phage-resistant)"
/clone_lib="NH1 MGC 191"
/clone_lib="NH1 MGC 191"
/note="Vector: phNR-LLB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BM919223
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteléostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1055)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Ungublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                               Homo sapiens (human)
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GI:19369602

bр О Ното

mRNA linear ES sapiens cDNA clone

EST 12-MAR-2002 ne IMAGE:5748442

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US-10-627-571-2 (1-188) x CD521721 (1-731)
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LysMetLeuAspGluGluAsnIle
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Best Local Similarity:
Query Match:
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plate: LLMM12776 row: d column: 11
High quality sequence stop: 677.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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TTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAAC
                            LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EccRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(BcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5748442"
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KEYWORDS
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183
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                                                                                                                                                                                                22 LysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeu
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Est strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA with a NotI-oligo(dT) primer. Five prime into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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On Feb 15, 2001 this sequence version replaced gi:31271310.
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AL549492
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       IleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPhe
                                                                                     GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGGCAGAGAAGATC
                                                                                                               AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
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/clone_lib="Ist strand cDNA was primed with a NotI-oligo(dT).
/note="Ist strand cDNA was primed with a cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CSODI044YG13"
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                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3485.f
For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO57AA04QPl&c=3485.f. Location/Qualifiers
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On Feb 15, 2001 this sequence version replaced
Contact: Genoscope
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AL550457 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens Clone CSODIO57YA07 5-PRIME, mRNA sequence.
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AL550457.3
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
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AL527566.3
                                2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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AL527566 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODCO24YA23 5-PRIME, mRNA sequence.
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                                                                                                                                                                                            On Feb 13, 2001 this sequence version replaced gi:31065417 Contact: Genoscope
                                                                                                                                                                                                                                 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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information about this cluster, see
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full-length cDNA clone Coof Homo sapiens (human).
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Liwas normalized. Library was constructed by Life Technologies, division of Invitrogen.
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http://fulllength.invitrogen.com/
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu
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 CATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTG
                                                                   TTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCA
                                                                                          LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer
                                                                                                                                                      ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu
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/db xref="taxon:9606"
/clone="CSODIO57YA07"
/tissue type="Placenta Cot 2
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.com/ InVitroGen Corp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2004) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTC; CNSLT_CDNA.
                                                                                                                                             LysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeu
 IleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPhe
                                                                         AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
                                                                                                                         AAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTG
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CSODC024YA23"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Direct Submission

Genoscope - Centre National de
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genos

Web : www.genoscope.cns.fr)
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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Homo sapiens (human)
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                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA,"
/db_xref="taxon:9606"
/clone="CSODIO81YO11"
/tissue_type="Placenta Cot 2
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1754
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                  source
                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13492 row: f column: 02
High quality sequence stop: 596.
location/Qualifiers
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AGENCOURT_7833747 NIH_MGC_67
5', mRNA sequence.
BQ424670
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 996)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Macaca mulatta
Macaca mulatta
                                                                    998 bp mRNA linear EST 13-MAY-2004 ILLUMGEEN_MCQ_30108 Katze_MMPB Macaca mulatta cDNA clone IEIUW:6795 5' similar to Bases 72 to 998 highly similar to human TNFAIP8 (Hs.17839), mRNA sequence.
                                                                                                                                                                                         LysMetLeuAspGluGluAsnIle 188
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/lab_host="DH108 (phage-resistant)"
/clone lib="NIH_MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
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/db_xref="taxon:9606"
/clone="IMAGE:6153217"
                                           GI:47161702
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Plate: CL000256 row
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Illumigen Biosciences.Inc.
2203 Airport Way S, Suite 450,
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. Large-scale Rhesus Macaque cDNA Sequencing Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cmagness@illumigen.com
Sequenced on 2004.03.27. 798 (
PCR PRimers
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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               MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                             ATCATCAAGAACCTTATCAAGACGGTCATCAAGCTGGCCATTCTTTACAGGAATAATCAG
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ATGACCGTGGTCAGTTTCCACCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
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/note="Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I /note="Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I /Created from Stratagene ZAP-cDNA Synthesis kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit
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/clone="IBIUW:6795"
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/mol_type="mRNA"
/strain="Indian"
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1 (bases 1 to 1045)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31275981.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                      N
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was dispetted with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                         /tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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mol_type="mRNA"
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Fobo,G., Han,M. and W
Pongo pygmaeus mRNA (
Unpublished (2004)
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                                                                               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wieman Molecular Genome Analysis, German Cancer Research Center (DKFZ) Email s. wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp469E1232) is available the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                 Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 779)
                                                                                                                                                                                                                                                                                                    Contact: MIPS
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/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469E1232"
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                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 876)
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/lab_host="pH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMAI1481 row: j column: 18
High quality sequence stop: 813.
Location/Qualifiers
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Tissue Procurement: Life Technologies,
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                                                      SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
                                                                                                                       LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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LeuTyrAsnPro-PheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAs 180
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki, Okumura,N., Hamasima,N. and Awata,T.

PEDE (Pig EST Data Explorer): construction of a data derived from porcine full-length cDNA libraries ducleic Acids Res. 32 (1), D484-D488 (2004)
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BP433798
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EST project with full-length enriched cDNA libraries carried out

Animal Genome Research Program (Japan) by National Institute of

Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627
Fax: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector sequences were eliminated by RepeatMasker version 2002/07/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 32 (1),
Contact: Hirohide Uenishi
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                     LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="LNG010079A10"
/tissue_type="lung"
/dev_stage="adult"
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Conservative:
Mismatches:
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Sus.
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                                                                                                                                                                                                                                                                             Intestinal Muscle and Epithel Unpublished (2004)
Contact: Richard G. Baumann Bovine Functional Genomics La ANRI BLDG 162: BARC-EAST, Beltsvil Tel: 3015048604
Fax: 3015048744
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CN789950
CN789950.1
EST.
                                                                                                                                                                                                       Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.00925 using options -trim att ' -trim fastaVector identified
cross match using options -minmatch 12 -minscore 12
plate: 35 row: M column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 669)
Baumann, R.G., Baldw
Matukumalli, L.K.
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Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                             primer: CCTATTTAGGTGACACTATAGAAC h quality sequence stop: 669.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                              162: BARC-EAST, Beltsville,
 /tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TONA"
/clone_lib="BARC 8BOV"
                                                          /db_xref="taxon:9913"
/clone="8BOV_35M20"
/sex="Female"
                                                                                                  /strain="Holstein"
                                                                                                                                  organism="Bos taurus"
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                                                                                                                    type="mRNA"
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8BOV_35M20 5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 942) NIH-MGC http://mgc.nci.nih.gov/.
                                                          Mus musculus
                                                                                                     CA984413.1
                                                                        Mus musculus (house mouse)
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/note="Organ: Intestine; Vector: pCMVSport6.1; Site 1: Not1; Site 2: EcoRI; Normalized cow cDNA intestinal library in pCMVsport6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"

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US-10-627-571-2 (1-188) x CN789950
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Best Local Similarity:
                                                                                                                              121 LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
           CA984413 942 bp

MGENCOURT 11295099 NIH MGC 164 Mus

IMAGE: 30146475 5', mRNA sequence.
CA984413
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Plate: NDAM0062 row: d column: 04
High quality sequence start: 21
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Tissue Procurement: Dr. David Rowe and Dr. Mina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                              MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                           LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                          TTCAATCAAGACGAGCTGGCGCTCATGGAGAAGTTCAAGAAGAAGGTGCACCAGCTTGCC
                                                                                                                                                                                                                             PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla 100
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                                                        CTGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTACCGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db xref="taxon:10090"
/clone="IMAGE:30146475"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 164"
/clone lib="NIH MGC 164"
/clone lib="NIH MGC 164"
/note="vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: Not1;
Non-normalized full-length enriched library from pooled
mouse embryonic limb, maxilla and mandble, day 10.5 and
11.5 (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: Oligo-dT. cDNA enrichment:
>lk bp, Average insert size 1.8k bp. Priming sequence:
5'GACTAGTTCTAGATCGCGAGCGGCCGCCC(T) 3'. Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp."
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924.00
98.94%
94.68%
96.05%
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REFERENCE
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
plate: LLAM11457 row: k column: 04
High quality sequence start: 5
High quality sequence stop: 869.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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603042814F1 NIH_MGC_116
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LysMetLeuAspGluGluAsnIle
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                                                                                                                                                                                                                                                                                    /clone_lib="NIH MGC_116"
//clone_lib="NIH MGC_116"
//note="Organ: pooled colon, kidney, stomach; Vector:
//note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5183355"
                                                                                                                                  4.94e-101
923.00
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95.95%
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Conservative:
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sapiens cDNA clone IMAGE:5183355 5',
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MY1 000178 Mouse 9-day fetus c:
cDNA clone ICRFp522C0838 5', mi
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BF607236.1 GI:13503728
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                                                          Tel: 449 30 8413 1612
Fax: 449 30 8413 1802
Email: hennig@molgen.mpg.de
EST's are made from clones being representatives of clone clusters.
Clone clusters were calculated from oligonucleotide fingerprints.
PCR PRimers
FORWARD: 5'-GAGCTATTCCAGAAGTAGTGA-3'
BACKWARD: 5'-TAATTAGGACTCACTATAGGG-3'.
Seq primer: 5'-ATTTAGGTGACACTATAG-3'
Seq primer: 5'-ATTTAGGTGACACTATAG-3'.
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                                                                                                                                                                                     Contact: Hennig S
Laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
                                                                                                                                                                                                                                                                       Yahyawi,M., Hennig,S., Neidhardt,L., Radelof,U., Hermann,B.G., Lehrach,H. and O'Brien,J.
Detection of a high number of novel genes in a 9-day mouse embryo CDNA library normalised by oligonucleotide fingerprinting Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 832)
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                                                                                                                                                                                                                                                                                                                                                                                                        musculus (house mouse)
     /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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AGENCOURT 10735591 NIH MGC 154 Mus

IMAGE:30122433 5', mRNA sequence.

CA469176 CA469176.1 GI:24925528
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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US-10-627-571-2 (1-188)
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Best Local Similarity:
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LysMetLeuAspGluGluAsnIle 188
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                                                                                                                          TCTCACGGACGGGTTAATAATGTCTTTGACCATTTTTCAGATTGTGATTTTTTGGCTGCC
                                                                                                                                               SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="ICRFp522C0838"
/tissue_type="whole embryo"
/dev_stage="embryonic 9-day"
/lab_host="E.coli, XII blue"
/clone_lib="Mouse 9-day fetus cDNA library ICRFp522"
/note="Vector: PSVSport1; Site 1: Not1; Site 2: Sall;
Library preparation by oligo_dT priming of RNA. Clones
be ordered from the Resource Center in Berlin,
http://www.rzpd.de."
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Tissue Procurement: Bradfield Laboratory
cDNA Library Preparation: Mark Bittinger
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDKM0025 row: j column: 10
High quality sequence stop: 578.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                   MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                                                                   MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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CTGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTACCGCCAAG
              LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                       ATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGG
                                                                                                              TTCAATCAAGACGAGCTGGCGCTCATGGAGAAGTTCAAGAAGGAGGTGCACCAGCTTGCC
                                                                                                                              PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla 100
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/db_xref="taxon:10090"
/clone="IMAGE:30122433"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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Query Match:

Similarity:

1.09e-100 920.00 98.94% 94.15% 95.63%

Conservative: Mismatches: Indels:

9 177 2 0

Score:

Pred. Alignment

No.:

US-10-627-571-2 (1-188) x BI525793 (1-865)

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RESULT 26
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
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                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11155 row: o column: 13
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information
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Ph.D.
                                                                                                                                                                                                                                                                            organism="Mus musculus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                            db_xref="taxon:10090"/
                                                                                                                                                                                                                                                          strain="CZECH II"
                                                                                                                                                                                                                          clone="IMAGE:5057508"
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                                                                      Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 WVY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 WVW cedex - France
Email: segrefogenoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 559)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31283006.

Contact: Genoscope
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AL558873
AL558873.3 GI:46184260
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                      For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ015DD02QPl&c=3485.f. Location/Qualifiers
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Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORWALIZED
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MPE06324, mRNA sequence.
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized
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/clone|line="Homo sapiens T CELLS"
/clone="Homo sapi
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US-10-627-571-2 (1-188) x AL558873 (1-559)
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(human)

macrophage

Homo sapiens

Project

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1 (bases 1 to 580)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims_u-tokyo_ac.jp.
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                                                                         ValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnProPheGlyAsn
                                                                                                                                                                                                                                                        MetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsn
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Best Local Similarity:
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David Segal Ph.D., Herbert Morse M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1478145
Seg primer: -40RP from Gibco
High quality sequence stop: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 651)
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                     LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln 80
                                                                                           LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                        GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                                                                                                                  MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                                                                                                                                                   GGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCGAGGTG
                                                                                                                                                                                                                              ATGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTG
GTCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCCTCCACAGGAACAATCAG
                                                                       CTAGATGAGCTGTACAGGGTGACCAAGGAGTACACCCAGAACAAGAAGGAGGCGGAGAGG
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Sp2"
/note="Organ: spleen; Vector: pCMV-SPORT6 (Life
Technologies); mRNA made from flow-sorted NK cells, cDNA
made by oligo-dT priming. Directionally cloned. Average
insert size 1.5 kb. Primary library, non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db xref="taxon:10090"
/clone="uMAGE:3978113"
/close="WK cells (flow-sorted)"
/tlssue type="NK cells (flow-sorted)"
/lab_host="DH10B (Tl-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                  Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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AU135377.1
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AU135377
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 816)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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                                                                                                                                                                                                                                 /organism="Homo
/mol_type="mRNA'
                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1001920"
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                          'tissue_type="placenta"
'clone_lib="PLACE1"
                                              3.08e-100
916.00
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96.84%
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                                                                                                  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
                                                                                   Genome Res.
20499374
                                                                                                                                                                                                   Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253
                                                                                                                                                                                                                                                                                                                                                                                         AK090316

1542 bp mRNA linear HTC 03-i
Mus musculus 14 days embryo lung cDNA, RIKEN full-length en
library, clone:G630049H02 product:TNF-INDUCED PROTEIN GG2-1
                                                                                                                                                                                                                                                                                      Eukaryota;
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HTC; CAP trapper.
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Rodentia;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

B 6 (bases 1 to 1542)

Radachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Haraoka, T., Hirozane, T., Hayashida, K., Hayatsu, M., Hiramoto, K., Hiraoka, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kotho, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in R. Genomic Sciences Center and Genome Science Laboratory in RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                                                                                                                                          /note="unnamed protein product; TNF-INDUCED PROTEIN GG2-1
homolog [Homo sapiens] (SPTR|Q9UP47, evidence: FASTY,
93.6%ID, 100%length, match=565)
                                                                                                                                                                                                                                                                                              /clone_Tib="RIKEN_full-leng
/dev_stage="14 days embryo"
118._.714
                                                                    /translation="mlseaeeprevatdvfnsknlavqaqkkilgkmvsksiattlid
dtssevldelyrvtkeytqnkkeaerviknliktviklavlhrnnqfnqdelalmekf
kkkvhqlamtvvsfhqveytfdrnvlsrllnecrellheiiqrhltakshgrvnnvfd
                                                    HFSDCDFLAALYNPFGKFKPHLQKLCDGIKKMLDEENI"
                                                                                                                                      /codon_start=1
/protein_id="BAC41167.1"
/db_xref="GI:26355503"
                                                                                                                                                                                                                                                                                                                                /tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="FANTOM_DB:G630049H02"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                  /clone="G630049H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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Eukaryota; Metazoa; Chordata; Crania Mammalia; Eutheria; Rodentia; Sciuro 1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mamma Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scores:
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US-10-627-571-2 (1-188) x BI688217 (1-908)
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                                                                                                                                                                                                                                                                                        MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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   LysMetLeuAspGluGluAsnIle
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                                           TTGTACAATCCCTTTGGAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGGCCTCAAC
                                                                 LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: NotI; Cloned unddirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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/tissue type="infiltrating ductal carcinoma"
/dev stage="5 months"
/lab_host="DH10B"
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/strain="FVB/N"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E.: Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM11869 row: b column: 12
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Tissue Procurement: Jeffrey Green M.D.
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National Institutes of Health, Mammalian
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LysIleLysAsnLeuIleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGln
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                                                                                                                                                           GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
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/tissue_type="infiltrating
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Mus musculus
Mus musculus
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BI103517
BI103517.1 GI:14554410
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 772)
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                                                                                                                                                                                                                                                                                                                                             e: LLAM11121 row: c column: quality sequence stop: 751.
Location/Qualifiers
                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:5044167"
/clone="IMAGE:5044167"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI_CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SpORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library. | "
                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
 3.52e-99
907.00
98.41%
93.65%
 Length:
Matches:
Conservative:
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CB991862.1
EST.
                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 785)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                             CB991862 785 bp rAGENCOURT 13618130 NIH MGC 148 Homo IMAGE: 30337918 5', mRNA sequence.
                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDAM363 row: 1 column: 23
                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                     nLysMetLeu-AspGluGlu 186
                                                                                                                                                     TCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
                                                                                                                                                                                                             CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
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                                         CAAAATGTTGGGATGAAGAG
                                                                                              TTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGGTGATGGTATCAA
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//note=Torgan: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: Bam#; Library is oligo-dT primed and
directionally Cloned using primer
5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-lenght clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
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1. .785
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30337918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lab_host="DH10B TonA"
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Nature 420, 563-573 (2002)

26 (bases 1 to 1836)

27 (bases 1 to 1836)

28 Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Muzaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y.
                                                             Direct Submission

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute or Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute or Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Haradda, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the RIKEN Group Phase I & II Team.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dhno,M., Ohsato,N.,
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Sciences

Center and Genome Science Laboratory in RIKEN.

Research Group in

Riken

FEATURES

and

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Please visit our web site for fur
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                      aMetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerAr
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               CTTGTACAATCCCTTTGGAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGGCATCAA
                               aLeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAs
                                                                                                                             GCTGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTACCGCCAA
                                                                                                                                             gLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLy
                                                                                                                                                                                        CATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAG
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/clone_Tib="RIKEN full-length
/dev_stage="0 day neonate"
226. .823
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(SPTR|Q9UP47, evidence: FASTY, 93.6%ID, 100%length,
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/mol_type="mRNA"

/strain="C57BL/GJ"

/db_xref="FANTOM_DB:E130304C20"

/db_xref="taxon:10090"
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AUTHORS
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Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
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Sun Yat-sen University
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LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys 140
                                          MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                   PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla
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                            ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="reaxon:9606"
/tissue_type="normal nasopharynx"
/clone_Tib="human nasopharynx"
/note="ESTS generated from a normal nasopharynx
library from southern Chinese"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                      GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                       MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
 GGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCGAGGTG
                                                                    GTGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5354281"
/sex="female, virgin"
/tissue_type="infiltrating
                                                                                                                                                                                                                                                                                                                                                                                                                                dev_stage="5 months"
lab_host="DH10B"
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                                                                                                                                                                                      http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469E2119
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wie Molecular Genome Analysis, German Cancer Research Center (DKF Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD
                                                                                                                                                                                                                                                                                                                                                                       Pongo pygmaeus mRNA
Unpublished (2004)
Contact: MIPS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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Pongo pygmaeus
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Mewes,H.W., Weil,B., A
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       /tissue_type="kidney"
/dev stage="adult"
/lab_host="DH10B"
/clome_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_]
                                                                                                    /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469E2119"
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              Site_1: SfilA;
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                                                                                                               Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 566)

Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li,S., Dricot, A., Li,N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Douelte-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, I
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                                                                                                                                                       CV023086 The CDNA from the Mammalian Gene Collection sapiens cDNA 5' similar to BC007014, mRNA sequence.
                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                       Contact: Vidal M
                                                                                                                                                                                                                                                                                                                                                                                  CV023086.1 GI:51480836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Marc_Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cl
results from a PCR reaction using an MGC full-length cDNA
template DNA and ORF specific primers
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 566 Std Error: 21.00
Plate: 11075 row: 05 column: F
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
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BACKWARD: CATATGTTCTCTTCATCCAACATTT
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                                                            SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                          LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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                                                                                                                     CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
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                                     TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue type="mixed"
/clone_lib="Full Length cDNA from the Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30548565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence belongs to sequence cluster 3485.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE013CE09QP1&c=3485.f.
Location/Qualifiers
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2 rue Gaston Cremieux, CP 5706 - 91057 EV
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                                                                                                                                                                                                                                        AlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGly
                     AAAAWGGTGTCCAAATCCATCGCCACCACCTTAAWARAMGACACAAGTAGTGAGGTGCTG
                                                                                                                                                                                                                     GCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAAAGATCTTGGGT
ATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAAWCAGTTT
                                                                     GATGAGCTCTACARAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGGCAGAGAAGATC 182
                                                                                            AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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898.00
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95.19%
93.35%
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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AGENCOURT 14360208 NIH MGC 191 Homo
IMAGE: 30410510 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 747)
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quality sequence stop: 499.
Location/Qualifiers
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/clone="IMAGE:30410510"
/tlissue_type="pooled"
/tlissue_type="pooled"
/lab host="DH10B (TI phage-resistant)"
/lab host="DH10B (TI phage-resistant)"
/clone lib="NIH MGC 191"
/clone lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
/intery is oligo-dT primed
and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/shour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0.kb). 15/15 colonies contained inserts
                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                              mol_type="mRNA"
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VERSION
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musculus cDNA clone I830
BY743355
BY743355,1 GI:27169364
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yadji,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                     1 (bases 1 to 671)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
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                                                                                                                                                                                                                                                        671 bp mRNA linear
RIKEN full-length enriched, bone marrow
cDNA clone I830007M06 5', mRNA sequence.
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Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, M., Jackson, I.J., Jarvis, E.D., Kanai, A.,
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Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Maltais, L., Chido, T., Pavan, W.J., Pertea, G., Pesole, G.,
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Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Raid, J. Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

NE 22344683
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                              Location/Qualifiers
db_xref="taxon:10090"
                                           'strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 739)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                     mRNA sequence. — — BF140519 BF140519.1 GI:10979546 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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601787536F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015160 5',
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                                                                                            musculus
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/clone_lib="RIKEN full-length
macrophage"
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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LysMetLeuAspGluGluAsnIle 188
                               LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn 180
                                                                                                                 SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
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                                                                                               TCTCACGGACGGGTTAATAATGTCTTTGACCATTTTTCAGA-TGTGATTTTTTGGCTGCC
                                                                                                                                                                                                                                                                                                    CTAGATGAGCTGTACAGGGTGACCAAAGAGTACACCCAGAACAAGAAGGAGGCGGAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 709.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="tumor, metastatic to mammary"
/lab_host="DH108"
/clone_lib="WCI_CGAP_Lu30"
/clone_lib="WCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; transgenic model WNT-1, expression driv
MMTV-LTR enhancer; Cloned unidirent conslly. Primer:
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
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Further information about the clone and the sequencing project is
available at http://mlps.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ordering:
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MIPS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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/mol_type="mRNA"
/mb_xref="texon:9600"
/clome="DKFZp46910535"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clome_lib="469 (synonym: pkid1)"
/note="Vector: pSportl_Sfi; Site_1: Sf
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1 (bases 1 to 1892)

Horrevoets,A.J., Fontijn,R.D., van Zonneveld,A.J., de Vries,C.J., ten Cate,J.W. and Pannekoek,H.

Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two nove
                                                                                                                                                                                                                                                  Similarity 99. 00; Conservative
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Horrevoets, A.J.G., Fontijn, R.D.
Direct Submission
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/protein_id="AAC83229.1"
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110 human secretory proteins Patent: UP 2002508167-A 107 19 HUMAN GENOME SCIENCES INC OS Homo sapiens (human) PN JP 2002508167-AA/107 PD 19-MAR-2002 PF 17-DEC-1997 US 60/068 057,18 18-DEC-1997 US 60/068 064,18 18-DEC-1997 US 60/068 064,18 18-DEC-1997 US 60/068 169,19 19-DEC-1997 US 60/068 169,19 19-DEC-1997 US 60/068 367,19 19-DEC-1997 US 60/068 367,19 19-DEC-1997 US 60/068 367,19 19-DEC-1997 US 60/068 365 PI PAUL A MOORE, STEVEN M RUB. PI PAUL A ROSEN,
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110 human secretory proteins.
BD135356
BD135356.1 GI:23230301
JP 2002508167-A/107.
Homo sariara /
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Moore, P.A., Ruben, S.M., Carter, K.C., Shi, Y., Ros Soppet, D.R., Caou, H., Wei, Y.F., Florence, K., Dua Florence, C., Greene, J.M., Feng, P., Ferrie, A.M.,
PC C12N15/09, A61K38/00, A61K48/00, A61P9/00, A61P9/10, A61P15/00, A61P25/00, A61P25/00, A61P25/00, A61P25/02, A61P25/14, A61P25/16, A61P25/18, A61P25/22, A61P25/2
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CHARLES FLORENCE, JOHN
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A61P25/02, A61P25/14, A61P25/16, A61P25/18, A61P25/22, A61P25/24,
                                                     IG YU,
FORD JANAT, JIAN
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JR 2000539040

G0/070 923,18-DEC-1997 US 6.60/068 057,18-DEC-1997 US 6.60/068 064,18-DEC-1997 US 6.60/068 165,19-DEC-1997 US 6.60/068 367,19-DEC-1997 US
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60/068 054 P
60/068 053 P
60/068 368 P
60/068 369 P
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Duan, R.D.,
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RESULT 3
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A61P29/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
A61P29/00,C07K14/47,C07K16/18,C12N1/15,G01N33/50,G01N33/53,C12N15/00, PC
C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,C12N15/00, PC
PC C12N5/00
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FT Key
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BD156880 Primer for synthesizing f
BD156880 BD156880.1 GI:27862638
JP 2002191363-A/11723.
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                                                                                                      TTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA
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Location/Qualifiers
1...1943
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 2.4e-136;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1921)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11723 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/11723
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10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
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28-JUL-2000 JF 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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KEIICHI NAGAI,TETSUJI OTSUKI
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 5.3e-136;
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Research Association for Biotechnology (JP)
Location/Qualifiers
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Sequence 12751 from Pat
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Mammalia; Eutheria; Primates;
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/db_xref="G1:40032583"
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/translation="marDvensknlavQaQkkiigkmvsksiattliddtssevldel
/translation="marDvensknlavQaQkkiigkmvsksiattliddtssevldel
YRVTREYTQNKKEAEKIIKNLIKTVIKLAILYRNNQFNQDELALMEKFKKKVHQLAMT
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/db_xref="taxon:9606"
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Pred. No. 5.3e-136;
0; Mismatches 2;
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3 (bases 1 to 1921)
Isogai,T. and Otsuki,T.
Direct Submission
                                                                                                              Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuk.
Nishikawa,T., Nagai,K., Sugano,S., Actsuka,S., Yoshikawa,Y.,
Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sasaki
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Homo sapiens cDNA FLJ11069 fis,
                                                                   Unpublished
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                                                                                             NEDO human cDNA sequencing
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BD156785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etc.) and Department of Virology, Institute of Medical Science. University of Tokyo.
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1 (bases 1 to 1729)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 11628 09-JUL-2002;

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/11628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer for synthesizing full-length cDNA and use thereof. bb156785 BB156785.1 GI:27862543 JP 2002191363-A/11628.
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                                                                                                            TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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KEIICHI NAGAI,TETSUJI OTSUKI
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Qy 96 GTANAATGGTGTCCAAATCCATCGCCACCCTTAATAGACGACACAAGTAGTAGTGAGGTGC	CDS 71.667 /db_xref="taxon:9606" /note="unnamed protein product" /codon starte=1 /protein_id="CAB89829.1" /protein_id="CAB89829.1" /db_xref="GI:40032410" /franslation="MHSEABESKEVATDVFNSKNLAVQAQKKILGKMVSKSIATTLID DTSSEVLDELYBVTREYTQNKKEABKIIGNLIKTVIKLAILYRNNQFNQDELALMEKF KKKVHQLAMTVVSFHQVDYTFDRNVLSRLLNECREMLHQIIQRHLTAKSHGRVNNVFD BTSSEVLDELYBVTREYTQNKKEABKIIGNLIKTVIKLAILYRNNQFNQDELALMEKF KKKVHQLAMTVVSFHQVDYTFDRNVLSRLLNECREMLHQIIQRHLTAKSHGRVNNVFD ORIGIN Query Match 93.9%; Score 564.4; DB 6; Length 1729; Best Local Similarity 99.8%; Pred. No. 2.2e-130; Matches 565; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 565; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 565; TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG 95	AX877673.1 G AX877673.1 G Homo sapiens Homo sapiens Eukaryota; Me Mammalia; Eut 1 Ota, T., Isoga Ishii,S., Sug Primers for sa Patent: EP 10 Research Assc Loca , /org	Db 582 TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA 641 Qy 576 AAATGTTGGATGAAGAGAACATATGA 601 Db 642 AAATGTTGGATGAAGAGAACATATGA 667 RESULT 7 AX877673 LOCUS AX877673 DEFINITION Sequence 12578 from Patent EP1074617. ACCERSION AX877673
Noguchi, S., Itchir, Shigeta, K., Senbar, Marakami, I., Noguchi, S., Itchir, Shigeta, K., Senbar, Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satch, T., Shirai, Y., Takahashi, Y., Nakagawa, X., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. TITLE Complete sequencing and characterization of 21,243 full-length numan cDNAs Nat. Genet. 36 (1), 40-45 (2004) PUBMED 14702039 REFERENCE 160gai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nakamura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nakamura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A. Unpublished 3 (bases 1 to 1729) 3 (bases 1 to 1729) 3 Usases 1 to 1729 3 Usases 1 to 1729 3 Suman cDNA sequencing project Submitted (16-FBB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomicsehri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	Nagahari, K., Wamanoto, Y., Salto, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikawa, B., Omura, Y., Abe, K., Kahihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Sano, S., Moriya, S., Moniyama, H., Satoh, N., Takamata, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, K., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Tanaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Tanaya, M., Tanaya, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Tanaya, M., Tanaya, M., Chibari, R., Kanaya, M., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Tanaya, M., Chibari, R., Kanakami, R., Kanaya, M., Kanaya, M., Chibari, R., Kanaya, R., Chibari, R., Kanaya, R., Chibari, R., Kanaya, R., Chibari, R., Kanaya, R., Chibari, R., Kanaya,	RESULT 8 AK001850 AK001850 AK001850 AK001850 AK001850 DEFINITION Homo sapiens cDNA FLJ10988 fis, clone:PLACE1001920, highly similar to Homo sapiens MDC-3.13 isoform 2 mRNA. ACCESSION AK001850 VERSION AK001850.1 GI:7023373 KEYWORDS Oligo capping; fis (full insert sequence). SOURCE Homo sapiens (human) ORGANISM EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,	Qy 456 CACATGGACGGGTTAATAATGTCTTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT 515

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clone_lib="PLACE1"
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                                                                                                                                                                                                                                                                                                                           gene
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
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MDC-3.13, SCC-S2"

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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsiah, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
MCKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Transitute. 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                     CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://r
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                  Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
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                                                                                                                                                                              http://www-shgc.stanford.edu (Dickson, Mark) mcd@paxil.stanford.edu
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    Unpublished
2 (bases 1 to 1915)
Nietfeld, W. and Meye
                                           Nietfeld, W. and Meyerhans, A.F. Identification of cellular factors of dendritic cells
                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1915)
                                                                                                                                                                AF099935
Homo sapiens MDC-3.13:
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AF099935.1 GI:3860092
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function, which are induced by tumour necrosis factor"
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HFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI"
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DTSSEYLDELYRVTREYTQNKEAEKLIKNLKTVIKLAILYRNNQFNQDELALMEKF
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HFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI"
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   Homo
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Patent: WO 0.2068579-A 12009 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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                                 AF099936
Homo sapiens MDC-3.13
AF099936
AF099936.1 GI:3860094
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Homo sapiens
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/mol_type="unassigned DNI
/db_xref="taxon:9606"
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156 TGGATGAGCTCTACAGAGTGACCAGAGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA
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Nietfeld,W. and Meyerhans,A.F.
Identification of cellular factors involved in the differentiatio
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Nietfeld, W. and Meyerhans, A.F.
Direct Submission
TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                          CACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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MTVVSFHQVDVIFDRNVLSRLLNECREMLHQIIQRHLTAKSHGRVNNVFDHFSDCEFL
AALYNPFGNFKPHLQKLCDGINKMLDEENI"
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/cell_type="adherent m
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Klausner, R.D., Collins, F.S., Wagmer, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Millahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lux, Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA secuences
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through
Series:
This clo
                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: b Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657123.

Location/Qualifiers
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CDNA Library Arrayed by: The I.M.G.E. CONSORTIUM (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tisue Procurement: ATCC
Tisue Procurement: ATCC
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Homo sapiens tumor necrosis factor, alpha-induced protein 8, mRNA
(cDNA clone MGC:12346 IMAGE:3930240), complete cds.
BC007014
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R. M.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                  /organism="Homo sapiens"
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                                              /tissue_type="Brain, primitive
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note="Vector: pDNR-LIB"
                              /lab_host="DH10B"
                                                                                                                        /clone="MGC:12346 IMAGE:3930240"
                                                                                          neuroectodermal"
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RESULT 14 AK097284

LOCUS DEFINITION

AK097284 2502 bp mRNA linear Homo sapiens cDNA FLJ39965 fis, clone SPLEN2027157, to Homo sapiens MDC-3.13 isoform 2 mRNA.

PRI 30-JAN-2004 highly similar

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/note="DUF758; Region: Domain of unknown function
(DUF758). Family of eukaryotic proteins with unknown
function, which are induced by tumour necrosis factor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="TNFAIP8 protein"
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/protein id="AAH07014.1"
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/db xxef="HocusID:25816"
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/translation="MMSCAEESKEVATDVFNSKNLAVQAQKKILGKMVSKSIATTLID
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/db xref="LocusID:25816"
237. .833
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HFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI"
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                                                                                                                                                                                                                            Submitted (04-JUI-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy. Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Isogai,T. and Yamamoto,J.
Direct Submission
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/clone="SPLEN2027157"
                                                                          organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                           ocation/Qualifiers
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                            Submitted (06-APR-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA (Dases 1 to 112626)

DOE Joint Genome Institute and Stanford Human Genome Cer
                                                                                                            2 (bases 1 to 112626)
DOE Joint Genome Institute.
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 112626)

DOE Joint Genome Institute and Stanford Human Genome Center.
Submitted (27-APR-2001) DOE Joint Genome Institute,
                  Direct Submission
                                                                                                 Direct Submission
                                                                                                                                           Unpublished
                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                              Homo sapiens
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AC035144
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/note="cloning vector: pME18SFL3"
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Homo sapiens chromosome 5
AC026795
AC026795.6 GI:15718543
HTG.
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On Apr 27, 2001 this sequence version replaced gi:7712094.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Ouality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
   Homo
               Homo
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                                                                                                                                                 AAATGTTGGATGAAGAGAACATATGA
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2220M12"
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Pred. No. 2.4e-130;
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Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 156277)
DOE Joint Genome Institute and Stanford Human
Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Direct Submission
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Submitted (24-MAR-2000) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459
3 (bases 1 to 156277)
DOE Joint Genome Institute and Stanford Human Genome Center.
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www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.4.
STS Content:
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Drive, Walnut Creek, CA 94598, USA
On Sep 21, 2001 this sequence version replaced gi:15383783.
Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute.
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TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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/mol_type="genomic DNA"
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/db_xref="taxon:9606"
/chromosome="5"
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Pred. No. 2.4e-130;
n. Mismatches 1;
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                                                                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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                                                            MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-JAN-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 158057)
Tomlinson,C. and Bielicki,L.
The sequence of Homo sapiens
Unpublished (2001)
    SOURCE INFORMATION:
Clone CTD-2293E22 i
                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-MAY-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) 99063792
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Sulston, J.E. and Wilson, R.
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                                                                                                                                                                                             restriction
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Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 158057)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_MS2293E22
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The library contains cloned DNA from human sperm. See: al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Genomics 34:213-8 (1996). The clone is available from R Genetics, Inc. (http://www.resgen.com).
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This sequence is the entire insert
Location/Qualifiers
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7920. .8106
/rpt_family="polypurine"
20419. .20468
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2532. .2575
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6329. .7499
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1964. .1996
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19548. .19664
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[4630. 14800
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[8238. .18436
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L5534. .17744
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7503._.7872
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2859: .2886
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|518. .1547
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/clone_lib="CTD"
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Kim et al.,
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/rpt_family="AT_rich"
20476. .20771
/rpt_family="Alu"
21591. .22250

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33458. .33570
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31939. .32107
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39956. .40148
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                                                                                                            family="L1"
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                                                                                                                                                                                                         _family="tRNA-Glu-GAG"
                                                                                                                                                                                                                             _family="AT_rich"
                                                                                                                                                                                                                                                   family="AT_rich"
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                      Score 564.4; DB 9;
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REFERENCE
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                                                                                                                                                                                                                                                                                             Unpubliance
(Dages 1 to 573)
(Dages 1 to 573)
(Pages 2 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 573)

Ebert, L., Schick, M., Neubert, P., Schatten, R., Henze, S. and Korn, B. Cloning of human full open reading frames in Gateway (TM) system
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                                                                 RZPD; RZPD0834H127D, ORFNo 1910
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H127D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry vector (pDONR201)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATGTTGGATGAAGAGAACATATGA 134902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is a part of a collection of human full length expression clones generated by RZPD.

This CDS has been cloned incl. stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase (TM) reaction. Additional sequence has been added in front of the start codon: att. AAAAAA GCA (GGC (ATG)).

The last base of the last coding triplett has been changed to T, which might lead to an amino acid change at the C terminus of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAACCCAGCTITCIT. .att. Compared to the reference sequence NM_014350 we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
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The stop cod
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 CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCCACCTCACTGCCAAGT
                                                                                                                                               TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                                                                                      TTÄATCAAGATGAGCTAGCATTGATGGAGAAATTTXAGAAGAAAGTTCATCAGCTTGCTA
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                                                                                                          TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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/db xref="GI:48116391"
/db xref="GI:48116391"
/translation="manatdvensknlavQaQkkilgkmvsksiattliddtssevld
/translation="manatdvensknlavQaQkkilgkmvsksiattliddtssevld
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mtvvsphqvdytfdrnvvlsrllnecremlhqiiqrhltakshgrvnnvfdhfsdcefl
aalynpfgnfkphlqklcdginkmldeeni"
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/clone="RZPD0834H127D"
/clone_lib="Human Full ORF Clones Gateway(TM) -
/lab_host="DH10B"
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Pred. No. 1.3e-129;
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98.9%;
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156 TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCCAAAAACAAGAAGGAGGACGAGAAGA
276 TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA 335
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1 (bases 1 to 816)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length DNNA and use thereof Patent: JP 2002191363-A 4238 09-JUL-2002;

HELIX RESEARCH INSTITUTE
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Primer for synthesizing full-length cDNA and use thereof FH
Location/Qualifiers
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                                                    TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTATAGGAATAATCAGT
                                                                                                        TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
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28-JUL-2000 JP 2000280990
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 3.4e
0; Mismatches
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Db 6 RESULT 20 AX869333 LOCUS DEFINITION ACCESSION VERSION VE	D Q D Q D Q D Q
SILT 20 SSILT 2	8 1 2 5 6 9 0 3 4
RESULT 21 AXO97884 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS AUTHORS AUTHORS AUTHORS	Db 4 Qy 5 Qy 5 Qy 5 Qy 5
AK097884 AK0061, AK0881, AK0861, AK0881, AK0861, AK0881,	

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TITLE
JOURNAL
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AUTHORS
TITLE
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Best Local Similarity 93.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Isogai, T. and Yamamo
                                                                                                                                                        TGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCT
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                   AACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATAT
                                                                                                   TTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTA
                                                                                                                                                                                                                                                                        TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYMU2004688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="cloning vector: pME18SFL3"
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/clone_lib="THYMU2"
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Pred. No. 1.8e-114;
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                                 Worley, K.C.
Direct Submission
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Rattus norvegicus
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus clone CH230-10A12, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 237561: contig of 237561 bp in length.

1 cocation/Qualifiers
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Baylor Plaza,
3 (bases 1 tc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version
The sequence in this assembly is a co
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Rat Genome Sequencing Consortium.
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vlor Plaza, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                /note="wgs contig"
complement(232422...2
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                  /note="wgs_end_extension clone_end:Sp6"
/note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                     end_sequence:BH303075"
76320. .79576
                                              end_sequence:BH303071"
234103. .235440
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/note="clone_boundary
clone_end:Sp6
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_xref="taxon:10116"
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1728)

2 1 (bases 1 to 1728)

2 1 (bases 1 to 1728)

3 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                          BC009090 1728 bp mRNA linear ROD 30-JUN-2004 Mus musculus tumor necrosis factor, alpha-induced protein 8, mRNA (CDNA clone MGC:11714 IMAGE:3965693), complete cds.
                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAG 494
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/note="wgs_end_extension
clone_end:T7"
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Pred. No. 9.4e-103;
0; Mismatches 83;
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                                                                                         ORIGIN
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Query Match
Best Local Similarity
Matches 490; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 17 Row: n Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1952736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.T., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Center
Center code: BCM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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73.9%; ilarity 86.6%; Conservative
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70. .666
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model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam1"
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                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                   gene="Infaip8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="Tnfaip8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Vector: pCMV-SPORT6"
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  0
Score 444.4; DB 10;
Pred. No. 2.3e-100;
0; Mismatches 76;
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pietre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, R., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Lindblad, Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Wguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 184327)
Birren,B., Nusbaum,C. and Lander,E.
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AC120859
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TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Menyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Submitted (05-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 5, 2004 this sequence version replaced gi:49035085. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Murphy, T., NeyLor, J., Nguyen, C., Nguyen, T., Nicola, N., Comnor, T., O'Donnell, P., O'Neil, D., Oliver, J., Raymond, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stobanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 184327) Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Handerson, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Liu, G., Liu, R., Lui, A., Mabbitt, R., Liu, G., Liu, R., Lui, A., Mabbitt, R.,	Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Romann, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission L. Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Dassel to 18432) Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Levine, R., Lindblad-Toh, K., Liu, S., Liu, A., Mathhews, C., Macchen, C., Macdonald, P., Major, J., Manning, J., Mathhews, C., Macchen, C., Macdonald, P., Major, J., Manning, J., Mathhews, C.,
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RESULT 25 AJ720906

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Direct Submission
Submitted (20-MAY-2004) Caldwell R.B., GSF
Submitted (20-MAY-2004) Caldwell R.B., GSF
Institut fuer Molekulare Strahlenbiologie,
1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
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AJ720906
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Caldwell, R.B.
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                          AGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATC
                                                                         TTTTAGATGAGCTCTACAGAGTGACGAAGGAATACACGCAAAAACAAAAAGAAGCAGAGA
                                                                                                  TGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCCAAAACAAGAAGGAGGAGGCAGAGA
                                                                                                                                              TTGGGAAAATGGTATCCAAGTCAATAGCAACTACTTTGATAGATGATACCAGCAGTGATG
                                                                                                                                                                             TGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGG
                                                                                                                                                                                                                   CAATGGCCACGGATGTCTTCAATTCAAAAAAGCTTGGCCATTCAGGCCCAGAAGAAGATCC
 AGATCATTAAAAACCTCATTAAAATAGTCCTCAAATTGGCAATTCTCTACAGGAACAATC
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YRVTKEYTQNKKBABKIIKNLIKIVLKLAILYRNNQFNQDEIALMEKFKKKVHQLAKT
VVSFHQVDYTFDRNFLSKLLNDCRELLHQIIQRHLTAKSHGRVNNVFDHFSDCEFLAA
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189. .755
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/product="hypothetical protein"
/protein id="CAG32565.1"
/db_xref="GI:53136472"
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/tissue_type="bursa"
/clone_lib="riken1"
/dev_stage="2 weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Gallus gallus"
|mol_type="mRNA"
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note="ORF1"
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Pred. No. 2.1e-91;
0; Mismatches 99;
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PATURES FEATURES SOURCE ORIGIN Query Match Best Local S Matches 422 Qy 1 Db 105	ACCESSION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 26 BD149633 LOCUS DEFINITION	B &	B &	Qy Db	Qy bb	Qy Db	Qy Db
pC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers 1897 FT source /organism='Homo sapiens (human)' Location/Qualifiers 1587 /organism="Homo sapiens (human)' ce /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" atch 65.7%; Score 394.6; DB 6; Length \$87; cal Similarity 96.6%; Pred. No. 6.5e-88; 422; Conservative 0; Mismatches 13; Indels 2; Gaps 2; 1 CTTCAGCCTCCCGCGCCCCTCCCCCCCCCAGATGTCTTTAATTCCA 59	BD149633.1 GI:27855391 BD149633.1 GI:27855391 JP 2002191363-A/4476. Homo sapiens (human) Homo sapiens (human) 1 (bases 1 to 587) Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 4476 09-JUL-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/4476 PD 09-JUL-2000 PF 28-JUL-2000 PF 28-JUL-2000 PF 28-JUL-2000 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI CLENIS/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC	BD149633 S87 bp DNA linear	573 ACAAAATGTTGGATGAAGAGAACATAT 599 	513 CCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCA 572	453 AGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTG 512	393 GGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACCTGCCA 452	333 CTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCA 392	273 AGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTG 332
Query M Best Lo Matches Qy Db Db Db Db Qy Db Qy Db Db	RESULT 27 AX869571 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURC ORIGIN	Db Qy	Qy	Qy Db	B &	D Qy	D Qy	Qy Db
/ Match Local Similarity 96.6%; Pred. No. 6.5e-88; Local Similarity	AX869571 AX869571 N Sequence 4476 from Patent EP1074617. N AX869571 AX869571.1 GI:40024434 Homo sapiens (human) M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. 1 J. Sogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamam Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. E 1 Isojai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamam Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 4476 07-PEB-2001; Research Association for Biotechnology (JP) Location/Qualifiers 1587 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		360 TGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGTTAAATGAATG	300 TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG	240 TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA	180 GGGAGTACACCCAAAACAAGAAGGAGGAGGAAGATCATCAAGAACCTCATCAAGACAG	120 CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGGTCTACAGAGTGACCA	60 AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG

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                                                                                                                                                                                                                                                                                                                                                               452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-SEP-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST/CBNA project.
This sequence is from a Xenopus Gene Collection (XGC) library, from a library constructed by Aaron M. Zorn. cDNA was prepared from RNA extracted from eggs. EcoRI-NotI cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI, Site 2: NotI
Host: Escherichia coli XII-blue.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amaya, B., Ashurst, J.L., Bonfield, J.K., Croning, M.D.R., Francis, M.D., Garrett, N., Gilchrist, M.J., Grafham, D.V., McLaren, S.R., Papalopulu, N., Rogers, J., Smith, J.C., Tay Voigt, J. and Zorn, A.M.
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                                                                                                                                                                                                          GTTCAGGCACAAAAGAAGATCTTGGGTAAAATGG----TGTCCAAATCCATCGCCACCACC 127
                                                                                                                                                                                                                                                                                                   CCGGCGCCGTCGCCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCC 70
                                                                                                                                                                                GTACAAGCCCAAAAGAAGTTCTTGGCAAGATGGCCTCATCAAAGTACATAGCAACATCC
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                                            ACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAG 247
                                                                                        CTTATTGACGATACAAGCGGTGAAGTTCTAGATGAACTGTACCAATTGACGAGGGAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1559)
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus tropicalis"
/mol type="mRNA"
/db_xref='taxon:8364"
/clone="TEgg053008"
/clone_lib="XGC-egg"
/dev_stage="egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             59.2%;
76.1%;
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                                                                                                                                                                                                                                                                                                                                                        Score 355.6; DB 5;
Pred. No. 3.9e-78;
0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
clone
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TEgg053o08.
                                                                                                                                                                                                                                                                                                                                                                                                  Length 1559;
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                                                                                                                                                                                                                                                                                                                                                          ω,
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                        310
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                    JOURNAL
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ORGANISM
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BC072904
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                                                                                                                                                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBMED
                                                                                                    Klausner, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodeegren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1193 bp
Xenopus laevis MGC80354 protein,
IMAGE:5074412), complete cds
BC072904
                       Klein, S. and Gerhard, D.S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic and genomic tools for Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Richardson, P.
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  Submitted (07-JUN-2004) National
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC072904.1 GI:49115085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCATACAGCGCCATCTCACGGCAAAGTCTCACGGACGTGTTAATAACGTGTTTGACCAC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTTGATCAT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCAAGAGAAAGGTCCATCAGCTGGCCATGACTGTGGTCAGCTTTTATCAGGTGGAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTCAGATTGTGAATTTTTGGCCTGCCTTGTATAATCCTTTTTGGGAATTTTAAACCCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTTTGACCGAAACGTGCTTTCCAAATTGTTAAATGAGTGCCGGGAGCTGCTCCATCAG
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                                                                 (bases 1 to 1193)
Institutes of Health, Xenopus
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mRNA (cDNA clone MGC:80354
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The NIH Xenopus Clifton, S.W.

VRT 03-AUG-2004

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Best Local
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                                                                                                                                                                                     189
    309
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                                                                                                                                                                                                                                                                                                          11 CCGGCGCCGTCGCCGACTCCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCC
                                                                                                                                                                                                                                                                                                                                                                      451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 152 Row: j Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutser, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Li Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mori Teika Olson, Diana Palnquist, Anca Petrescu, Anna Lisa Prabbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Genome Sequence Cent:
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project
Contact: XGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development, 610
20892-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                           ACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAG
                                                                                                                                                                                   GTACAAGCCCAGAAGATTCTTGGCAAGATGGCTTCATCTAAATACATAGCAACGTCC
                                                                                                                                                                                                                              GTTCAGGCACAAAAGAAGATCTTGGGTAAAATGG---TGTCCAAATCCATCGCCACCACC
                                                                                                                                                                                                                                                                           CCCGCCCCAGGTGCCGCTGAGCCAATGGCAACCGATATCTTCAATTCCAAAAACCTGGCT 188
  ACCCAGAACAAGAAGGATGCCGAGAAAATCACAAAGAACCTCATCAAAACAGTCATCAAG
                                                                                          CTGATTGATGATACAAGTGGCGAAGTTCTAGATGAACTCTACCAAGTGACTAGGGAGTAC
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="LocusID:443963"
/translation="matdifnsknlavqaqkkilgknasskyiatsliddtsgevlde
Lyqvtreytqnkkdaekitknliktviklavlyrnnqfneeeiglmekfkrkvhqlam
TVVSFYQVEYTEDRNVLSKLLMECRELHQVIQRHLTAKSHGRVNNVFDHFSNCEFLA
ALYNPFGPYKKHLQRLCNGVNKMLDEDNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="MGC80354 protein"
/protein_id="AAH72904.1"
/db_xref="G1:49115086"
/db_xref="G1:49115086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MGC80354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Vector: pCMV-SPORT6"
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="MGC80354"
                                                                                                                                                                                                                                                                                                                                                                                            58.9%;
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                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                         Score 354; DB 5;
Pred. No. 9.7e-78;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 1193;
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368
                                             247
                                                                                          308
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298 GATGGAGAAATTTAAGAAGAAAGTTCATCATCATCATCTATGACCGTGGTCAGTTTCCATCA

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REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
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Query Match
Best Local Similarity
Matches 304; Conserv
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens head and neck tumor and metastasis related mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 515)

Kumar, D., Whiteside, T.L. and Kasid, U.
Identification of a novel tumor necrosis factor-alpha-inducible gene, SCC-22, containing the consensus sequence of a death effects domain of fas-associated death domain-like interleukin-
                                                                                                                                                                                                                                                                                                                             Submitted (14-OCT-1998) Radiation Medicine, Georgetown University, 3970 Reservoir Road NW, Washington, DC 20007, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                        Kumar,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1beta-converting enzyme-inhibitory protein J. Biol. Chem. 275 (4), 2973-2978 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTTTGACCGAAACGTGCTTTCCAAATTGTTAAACGAGTGCAGGGAGCTGCTTCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTTCCATCAGGTGGATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTCAAATTGTGAATTTTTAGCTGCTCTGTACAATCCCTTTGGACCTTACAAAAAAACAC
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     and Kasid, U.
                                                                                                                                                                   protein"
                                                                                                                                                                                                                    tissue type="head and neck squamous carcinoma"
                                                                                         /translation="mekfkkkkyhQlamtvvsfhQvDytfdrnvlsrllnecremlhQI
[QrhlTakshGrvnnvfdhfsdceflaalynpfgnfkphlQklcdGInkmldeenI"
                                                                                                                             /protein_id="AAF29435.1"
/db_xref="GI:6851133"
                                                                                                                                                                                product="head and neck tumor
                                                                                                                                                                                                   codon_start=2
                                                                                                                                                                                                                                                          db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                               .515
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               100.0%;
                                                                                                                                                                                                                                                                       _type="mRNA"
 0
               Score 304; DB 9;
Pred. No. 3.1e-65;
 Mismatches
                                                                                                                                                                                  and metastasis related
                                Length 515;
 Indels
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AUTHORS
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SOURCE
ORGANISM
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JOURNAL
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                                                                                                                                                                                                    CE 2 (bases 1 to 164258)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Chang, J., Chang, J., Chang, J., Cooke, P., Brown, A., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., KcEwan, P., McKerran, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connort, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wi, X., Wyman, D., Ye, W.J., Young, G., Zaihoun, J., Zembek, L., Zimmer, A. and Zody, M.

Blirren B., Nubhaum, C., Lander, R., Abouelleil a. Allen N.

Birren B., Nubhaum, C., Lander, R., Abouelleil a. Allen N.

Birren B., Subramanian, A., Lander, R., Abouelleil a. Allen N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus, clone RP24-174015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Ro
1 (bases 1 to 164258)
Birren,B., Nusbaum,C.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Mus musculus clone RP24-174015, WORKING DRAFT SEQUENCE, 8 unordered
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                                                                                                                         Choepel, Y.,
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap; version 0.960731
Consensus quality: 162506 bases at least Q40
Consensus quality: 162955 bases at least Q30
Consensus quality: 163183 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 164558; sum-of-contigs
Quality coverage: 11.0 in Q20 bases; sum-of-contigs
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104630
115027
115127
115127
131678
131778
158794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center Center code: WIBR
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37790
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29808
32341
32441
   clone_end:SP6
                                                                    /clone_l1
1. .29707
                               /note="assembly_fragment
                                                                                                                         db_xref="taxon:10090"
clone="RP24-174015"
                                                                                                                                                                                                                                                                         ocation
                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                   .164258
                                                                                                                                                                                                                                                                                                     158793: contig
158893: gap of
164258: contig
                                                                                                                                                                                 _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                  104629: gap of 100 bp
115026: contig of 10397 bp in length
115126: gap of 100 bp
131677: contig of 16551 bp in length
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32340:
                                                                                                                                                                                                                                                                                                                                                                   131777: gap of
158793: contig
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.04529: contig of 66740 bp
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37689: contig of 5249 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29707:
                                                                                                lib="RPCI-24 Male Mouse
                                                                                                                                                                                                                                                                            /Qualifiers
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contig of 2533 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 29707 bp in length
                                                                                                                                                                                                                                                                                                     100 bp
of 27016 bp in length
100 bp
of 5365 bp in length.
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RESULT 32
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                                       KEYWORDS
                                                                         VERSION
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Best Local S
Matches 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 TCCGATGGCCACAGATGTCTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
375; Conserv
                                                                                              AC107848 195574 bp D. Mus musculus chromosome 9 clone RP23 IN PROGRESS ***, 8 unordered pieces. AC107848
         AC107848.5 GI:45598920
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAA
                                                                                                                                                                                                                                                                                                                                    CAATAAATTGTTAGACGACAAGATCCTCTGA 87437
                                                                                                                                                                                                                                                                                                                                                                        CAACAAAATGTTGGATGAAGAGAACATATGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTCTCTATGGTCCGCATGGAAACTGCAGGCCCAATCTCAAGAGGATTTGCGAAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCTTGTATAATCCTTTTGGGAATTTTTAAACCCCCACTTACAAAAACTATGTGATGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAGCTTCTGCATGAGTGCAAGGACCTGGTACATGAACTGGTACAGCGACACTTGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAAATTTAAGAAGAAAGTTCATCAGCT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCTTTGATGAGCTGTACAAAGTCACAGAAATACACACCCACAACAAGAAGGAGGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGA
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ilarity 65.7%;
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37790. .104529
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32441. .37689
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158894. .164258
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131778. .158793
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104630. .115026
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[15127. .131677
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0; Mismatches 196;
                                                                                                                                               195574 bp DNA linea
ne 9 clone RP23-321A19 map
                                                                                                                                                     linear
9 map 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE 3 (bases 1 to 195574)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H.M., Barra, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barra, N., Bastien, V., Bloom, T., Boughslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Midota, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Madota, J., Malova, T., Mlenga, V., Murphy, T., Naylor, J., Maclin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Maclin, J., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stobbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., God, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McClean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Meßwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., McBwan, C., McCartnan, K., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Myuyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahinoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                Submitted (22-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2004 this sequence version replaced gi:44886703.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 195574)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mus musculus chromosome 9, clone RP23-321A19
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 195574)
                                                                                                                    Center project name: L20615
Center clone name: 321_A_19
                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L20615
                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center Center code: WIBR
                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                 ---- Genome Center
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CAACAAAATGTTGGATGAAGAGAACATATGA
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                                                                                                                                                       CAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGC
                                                                                                                                                                                                          TAAGCTTCTGCATGAGTGCAAGGACCTGGTACATGAACTGGTACAGCGACACTTGACACC
                                                                                                                                                                                                                                                                                     TGCGATGACCATGGTCAGCTTCTACGAAGTAGAGTATACCTTTGATACGAATGTGCTCTC
                                                                                                                                                                                                                                                                                                                                                              ACAGTTCAGTCAAGAGGAGGTTATAATTGTGGAGAAAACTCCGGAAGAAACTGAACCAGAC 160288
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                                                                                            TGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTAT
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/clone_lib="RPCI-23 Female Mouse
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28230: contig of 20252 bp in length
28230: gap of 100 bp
59488: contig of 31158 bp in length
59588: gap of 100 bp
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Pred. No. 1.7e-53;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Director MGC Project.
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                                                                                            /strain="AB"
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Strauberg, R.L., Peingold, B.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and monital analysis of more than 15,000 full-length

buman and monitse CNNA semences
                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 101 Row: c Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 41056158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sunio Sugano and Dr. Ko-ich
cDNA Library Preparation: Dr. Sunio Sugano and Dr.
cDNA Library Preparation: Dr. Sunio Sugano and Dr.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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3986 bp mRNA linear VRT 1
Danio rerio tumor necrosis factor, alpha-induced protein
(cDNA clone MGC:55331 IMAGE:2601021), complete cds.
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Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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/db_xref="taxon:7955"
/clone="MGC:55331 IMAGE:2601021"
/tissue_type="Whole body, adult,
including unfertilized eggs)"
/clone_lib="Sugano Kawakami zebra
                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/mol_type="mRNA"
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               BX649252.7
HTG.
 Danio rerio (zebrafish)
                                                           complete sequence
                                                                           Zebrafish DNA sequence from clone
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                                                                                                                                                                    GCTGGACGAAGGCAATCTTTGA 756
                                                                                                                                                                                                  GTTGGATGAAGAGAACATATGA 601
                                                                                                                                                                                                                                 CGGACCTTCAGAAGTGTACCGCGGCCACTTGCAGAAGATCTGTGAAGGAGTCAACAAGAT
                                                                                                                                                                                                                                                            TAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACAAAAT 579
                                                                                                                                                                                                                                                                                                                        TGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAAATTTTTGGCTGCCTTGTA 519
                                                                                                                                                                                                                                                                                                                                                       CAATGACTGCCGTGAACTTCTGCACCAGGCCATCAATCGGCATCTAACGGCGAAATCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="tumor necrosis factor, alpha-induced protein 8"
/protein id="AAH52765.1"
/db_xref="GI:31127058"
/db_xref="LocusED:393303"
/translation="MDSFSTKNLALQAQKKLMSKMATKTVANLFIDDTSSEVLDELYR
VTKEYTRNRKEAQKIIKNLIKNVVKLGVLYRNGQFNNEELALVERFRKKVHTLAMTAV
SFYQIIDFTFDRRVMSNLLNDCRELHQAINRHLTAKSHARINHVFNHFADCDFLATLY
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/db_xref="LocusID:393303"
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                               GI:42454788
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                                                                           DNA linear
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                                                                                         VRT 06-FEB-2004
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Query Match
Best Local Similarity
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone, and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where submirted.
                                                                                                                                                                                                            69467 GATGGCGACCAAGACAGTGGCCAACCTCTTTATAGACGACACCAGCAGCGAGGTACTGGA
                                                                                                                                                                                                                                                    100 AATGGTGTCCAAATCCATCGCCACCACCACCACGACGACGACGACACAAGTAGTGAGGTGCTGGA 159
220 CAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTATAGGAATAATCAGTTTAA 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 205949)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-49M19 is from a Zebrafish BAC library
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                                                                CGAGCTGTACAGAGTCACCAAAGAGTACACGCGCAACCGCAAGGAGGCCCAGAAGATCAT
                                                                                                                  TGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGATCAT
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/db_xref="taxon:7955"
/clone="DKEY-49M19"
/clone_lib="DanioKey"
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Pred. No. 3e-
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AC012678
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                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (03-NOV-1999) DNA Sequencing and Technology Center,
Submitted (University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                        Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 18837)
Bruno,D., Conn,L., Dela Rosa,M., Federspiel,N., Foreman,P.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
                                                                                                                                                                                                                                                                            Center
                                                                                                                                                                                                                                                                                                                                On Jan 21, 2000 this sequence version replaced gi:6223629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCULLO78
HOmo sapiens chromosome 15 clone SEQUENCE, 10 unordered pieces.
ACO15679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu,S. and Davis,R.W. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC012678
Center project Information
Center project name: 698
Center clone name: RP11-394B5
Center clone name: RP11-394B5
Sequencing Vector: Midmpl8; X02513
Sequencing Vector: Midmpl8; X02513
Chemistry: Dye primer; 0% of reads
Chemistry: Big Dye Terminator; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177081 bases at least Q40
Consensus quality: 185332 bases at least Q30
Consensus quality: 186766 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 188937)
                                                                                                                                                                                                                Web site: http://sequence-www.stanford.edu/group/human/Contact: hum-info@sequence.stanford.edu
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                                                                                                                                                                                                                                                                                                                              51681 TACCATAGGTCCTGATGTTTTTAGTTCAAAGAGTCTTGCGCCTTCAAGCCCAGAAGAAGAT 51740
                                                                                                                                                                                                  271 TCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAGTTCATCAGCT 330
                                                                                                                                                                                                                                                                                      211 GAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374;
                          CAATCTCCTGCATGAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGGCACCTGACGCC
                                                        CAGGCTGTTAAATGAATGCAGAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGC
                                                                                                                                      TGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATC
                                                                                                                                                                          CCAGTTTAGCCAAGAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGAC 51980
                                                                                                                                                                                                                                                    CAAGATCATGAAAGACTTAATCAAGGTGGCGATCAAAATCGGGATCCTCTACCGGAACAA
                                                                                                                                                                                                                                                                                                                                                              GGTGCTGGATGAGCTCTACAGAGTGACCAGGGGAGTACACCCCAAAACAAGAAGGAGGCAGA 210
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2221
7219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/chromosome="15"
/clone="RP11-394B5"
/clone_1ib="RPCI human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
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65.5%;
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138958: contig of 45433 bp in
139008: gap of unknown length
188937: contig of 49929 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 255.8;
Pred. No. 4.2
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Indels

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51860

51920

450

52040

52100

Length 188937;

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Insert size: 185828; agarose-fp
Insert size: 188487; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.2 in Q20 bases; sum-of-contigs.
**NOTE: This is a 'working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                   26919: gap of unknown length
39746: contrig of 12827 bp in 18
39766: gap of unknown length
54669: contrig of 14873 bp in 18
54719: gap of unknown length
69871: contrig of 15178 bp in 18
69947: gap of unknown length
93475: contrig of 23528 bp in 18
                                                                                                                                                                                                                                                                                                         2170: contig of 2170 bp in length
2220: gap of unknown length
7218: contig of 4998 bp in length
7268: gap of unknown length
15972: contig of 8654 bp in length
15972: gap of unknown length
26869: contig of 10897 bp in length
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length
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RESULT 36
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On Fe
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Submitted (23-FEB-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 189796)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom, Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Mad Nesbitt,R., Traicoff,R. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, Nesbitt, R., Traicoff, R. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-JUL-2000) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
AC073964
                                                                                                                                                                                                    and AC012169 [drafting
                                                                                                                                                                                                                     Note: Date from overlapping BACs AC022407 [drafting center: UWMCS]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing of human chromosome 15 D15S146-D15S117 region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feb 23, 2001 this sequence version replaced gi:9958002.
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                                                                                                                                                                                                                                                      Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of
Chemistry: Dye-primer Big Dye; 10% of read
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                           Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen0systemsbiology.org
Drafting center: SDSTDC
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                    Center: Multimegabase Sequencing Center Center code: UWMSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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/map="15q21.2"
/clone="RP11-394B5"
/clone_lib="RPCI human BAC library 11"
/note="Data from overlapping BACs RP11-105D1
                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                  1. .189796
                                                                                                                                                               ocation/Qualifiers
                                                                            chromosome="15"
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ne 15 clone
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                    Sequence 22:
CQ736656
CQ736656.1
                                                                      CQ736656
                                                     1248 bp DNA
22590 from Patent WO02068579.
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67852 CAATAAGTTGCTAGATGAGAAAGTCCTTTAA 67822
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                                                                                                                                                              CAACAAATGTTGGATGAAGAGAACATATGA
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17935. 17940
/note="low quality data"
55786. .56417
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/note="low quality data"
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105973
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161495 .161500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="low quality data"
104690. .104715
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Pred. No. 4.2e-53;
0; Mismatches 197;
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                                              CQ841622
Sequence 269 from Patent
CQ841622
CQ841622.1 GI:50893409
               Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 02068579-A 22590 06-SEP-2002; PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                           GTCTGGATGGAGACTGTAGGCCCAACCTCAAGAGGATTTGTGAAGGAATCAATAAGTTGC
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                                                                                                                                             TAGATGAGAAAGTCCTTTAA 1248
                                                                                                                                                                   TGGATGAAGAGAACATATGA 601
                                                                                                                                                                                                                  ATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGT 581
                                                                                                                                                                                                                                         GGCGCATCAACCACGTCTTTAACCACTTTGCCGATGTGGAGTTCCTCCTCCACCCTCTATA
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                                                                                                                                                                                                                                                                                          ATGAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGGCACCTGACGCCCAGGACCCACG
                                                                                                                                                                                                                                                                                                                  ATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATG
                                                                                                                                                                                                                                                                                                                                                                                                             AAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAAGTTCATCAGCTTGCTATGACCG
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                       Patent
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Pred. No. 8.2e-53;
0; Mismatches 191;
                                                                        1986 bp
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Ota, T.,
                                                                                             AK123281
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                                                                                                                                                                                                                  TGGATGAAGAGAACATATGA
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Nakagawa, S.,
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 Senoh, A.,
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AK123281.1 GI:34528784
oligo capping; fis (full insert
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                               AK123281 1986 bp mRNA linear Homo sapiens cDNA FLJ41287 fis, clone BRAMY2038484, similar to Homo sapiens MDC-3.13 isoform 2 mRNA.
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.
Full-length human cdna
Patent: EP 1440981-A 269 28-JUL-2004;
Research Association for Biotechnology (JP)
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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Pred. No. 8.3e-53;
0; Mismatches 191
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Mizuguchi, H.,
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Inagaki, H.,
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                                                                       Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatrari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. Sugno, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAB; annotation: HRI and RAB.
Location/Qualifiers
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                                     ATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCCACCTCACTGCCAAGTCACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGATGTTTTAGTTCAAAGAGTCTTGCGCTTCAAGCCCAGAAGAAGATTCTGAGCAAAA
                                                                                                TTGTCAGCTTCTATGAGGTGGAATACACCTTCGATAGGAACGTGCTCTCCAATCTCCTGC
                                                                                                                                     TGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGTTAA 401
                                                                                                                                                                                                      AAGAGGAGCTGGTTATTGTGGAGAAGTTCCCGGAAGAAGCTGAACCAGACCGCCATGACCA
                                                                                                                                                                                                                                                         AAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCG
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ATGAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGGCACCTGACGCCCAGGACCCACG
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/db_xref="GI:34528785"
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INHVFNHFADVEFLSTLYSLDGDCRPNLKRICEGINKLLDEKVL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_Tib="BRAMY2"
/note="cloning vector: pME18SFL3"
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/clone_lib="BRAMY2"
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Gallus gallus mRNA for hypothetical protein, clone 15i14.
AJ720336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M. Full-length cDNAs from bursal lymphocytes to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caldwell, R.B., Kierzek, A.M., Arakawa, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Submitted (20-MAY-2004) Caldwell R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                              /codon_start=1
/product="hypothetical protein"
/protein_id="CAG31995.1"
/bctein_id="CAG31995.1"
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/translation="MDTFSTRILALQAQKKILSKMASKTVANVFIDDTSSEILDELYR
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SFHQIDFTFDRRVVSSVLTECROLLHQAVSSHLTAKSHSRINHVFNHFADYEFLSALY
GPAEFYRTHLKRICEGVNKMLEEDNI"
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/strain="CB"
                                                                                                                                                                                                                                                                                      'note="ORF1"
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                                                                                              locus_tag="RCJMB04_15i14"
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Score 252.4; DB 5;
Pred. No. 2.6e-52;
0; Mismatches 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zaim, J.,
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WPCOMMENT 1/c
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Continuation (2
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Best Local Similarity
Matches 372; Conserv
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AC115187 3
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                        CCCACAAGATCATGAAGGATGTAATAAAGGTGGCGATCAAAATTGGTATTCTCTACCGGA
                                                                         CAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTATAGGA
                                                                                                                                                                            GTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGG
                                                                                                                                                                                                                                                                           AGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCATCTTAATAGACGACACAAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTACCGAGCCACGAAGGAGTACACTCACAATCGCAAAGAGGCCCAGAAGATCATCAAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GТGТССАРАТССАТССССАСССТТАЛТАСАССАСАСАСАСТАСТАСТСАССТССАСТСЯ В 163
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300001
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64.7%;
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310000
410000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
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AUTHORS
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AC115505/c
LOCUS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blswalo, K., Blair, J., Blankerhurg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dugan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garria, T., Garza, M., Gebregoorgia, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guwarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hernandez, R., Kally, S., Manden, S., Lopez, J., Lovez, J., Lovez, J., Lovez, J., Lovez, J., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Pully, M., Nair, L., Martin, K., Martin, K., Martin, K., Parks, K., Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32467
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCCACTCTCTACAGTCCGCACGGAAACTGCAGGCCCAATCTCAAGAGGATTTGCGAAG 32348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATG 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCCAGAACCCACGCACGCATAAACCATGTCTTCAACCACTTCGCTGATGTGGAATTCC 32408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAAACAGTTCAGTCAAGAGGAGGTTGTGATTGTGGAGAAACTCCGGAAGAAACTGAACC
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le CH230-77C4,
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, *** SEQUENCING IN PROGRESS
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Popovic, D.,

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 23, 2002 this sequence version replaced gi:23269911. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 256285)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-77C4
Center clone name: CH230-77C4
Center clone name: CH230-77C4
Center clone name: CH230-77C4
Center clone name: Phrap; version 0.990329
Consensus quality: 199255 bases at least Q40
Consensus quality: 203424 bases at least Q30
Consensus quality: 203424 bases at least Q20
Consensus quality: 203499 bases at least Q20
Estimated insert size: 195822; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
   24558
24658
201811
201911
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201910:
214313:
24557: contig of 24557 bp in length 24657: gap of unknown length 201810: contig of 177153 bp in length 201910: gap of unknown length 214313: contig of 12403 bp in length
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GTATCAACAAAATGTTGGATGAAGAGAACATATGA 601
                                                      TTTCCACTCTACAGTCCGCACGGAAACTGCAGGCCCAATCTCAAGAGGATTTGCGAAG 120073
                                                                                                                                          CGCCCAGAACCCACGGACGCATAAACCATGTCTTCAACCACTTCGCTGATGTGGAATTCC 120133
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                                                                                             TGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATG
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245270. .247000
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                                                                     JOURNAL
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Submitted (30-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                               Worley, K.C.
Direct Submission
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Rattus norvegicus clone CH230-112K14,
                                                                                                                                                                                         Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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                                 ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:23264293. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: CH230-112K14
Centendry Statistics
Assembly program: Atlas 3.0;
Consensus quality: 224959 bases at least Q40
Consensus quality: 227786 bases at least Q30
Consensus quality: 229294 bases at least Q20
Estimated insert size: 236137; sum-of-contigs estimation
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268970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                      complement (4198.
                                                                                                                                                                                        /clone="CH230-112K14"
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                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                          ocation,
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                                                  _sequence:BH258362*
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D. Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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Xenopus laevis MGC83729 protein,
IMAGE:6639647), complete cds.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                          and Richardson, P.
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                                                                                                                                                                                                                                        Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 1938)
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                                                                                                                                                                                                                       S.L., Strausberg, R.L., Wagner, L.,
                                                                                                                                                                                       and genomic tools for Xenopus
                                                                                                                                                       225 (4), 384-391 (2002)
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                                                                                                                                                                                        research:
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COMMENT
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Submitted (06-JUL-2004) National Institutes of Health, Xenopus Gene Submitted (08C), National Institute of Child Health and Human Collection (XGC), National Institute of Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 158 Row: d Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Teai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Contact: XGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@bcgsc.bc.ca
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RVFNHFADVEFLTALYSLEGNYRPYLKRICEGVNKLLDERVL"
                             /translation="MDTDSGDLSEGELSPGPEQFSSKSFAVQAQKKILSKMATKTMAN
MLIDDTSSEIFDELFKVTKEYVKNKKBAHKVLKDLVKVAVKVGILYRNKQFSLEELEI
VENFRKKLNQTCMTAVSFFEVEYTFDKNVLSGLLHECKTLLHELVQRHLTPKSHSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                   /product="MGC83729 protein"
/protein_id="AAH76797.1"
/db_xref="GI:49899743"
/db_xref="LocusID:446389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1938
                                                                                                                                                                                                                                                                                                               /gene="MGC83729"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                 db_xref="LocusID:446389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="Vector:
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ne_lib="NICHD_XGC_OO1"
host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 (26), 16899-16903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven L. Klein,
nologies, Inc.
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    TITLE
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            RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full length
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1 (bases 1 to 1813)
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Generation and initial analysis of more than 15,000
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  full-length
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  224 AACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAA 283
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Matches 346;
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Best Local Similarity
                                                           44 GATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: The I.M.A.G.E. Consortium (DNA Sequencing Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, when site:

http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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GCCACCATGGCCGTGGCGAACCTCCTAACAGACGACACCAGCAGCAGCAGATTCTGGACGAA
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HVFNHFADVDFLTELYGPSEDYRLNLRKICDGINKLLDEGTL"
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(protein id="AAH53167.1"
(db_xref="GI:31418811"
(db_xxef="GI:31418811"
(db_xxef="GI:31393322"
(db_xxef="MDSDSGEQSEGELSPGHESFNSKSLALQAQKKILSKMATMAVAN
/translation="MDSDSGEQSEGELSPGHESFNSKSLALQAQKKILSKMATMAVAN
/translation="MDSDSGEQSEGELSPGHESFNSKSLALQAQKKILSKMATMAVAN"
/translation="MDSGEQSEGELSPGHESFNSKSLALQAQKKILSKMATMAVAN"
/translation="MDSGEQSEGELSPGHESFNSKS"
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/db_xref="LocusID:393322"
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/tissue_type="Kidney, zebrafish"
/clone_lib="WCI_CGAP_ZKid1"
/lab_host="DH10B"
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Pred. No. 1.5e-45;
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CTCTACAGAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGGCAGAGAAGATCATCAAG

Db 409 GATGTCATCAAGATCGCTCTGAAGATTGGCATTCTTACCGGAACCACCAGTTCATCATCATCATCAGTCCTT Qy 284 GATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCCTTGCTATGACCGTG Q) 469 GAGGAGATGGAGACAGTGGAGCGCTTCCAAAAAGATGAAACCAACC
CCACCAGTTCAGTCCT 468 GCTTGCTATGACCGTG 343 G

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Maximum Match 100%
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(without alignments)
7490.031 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Acc81105 Human TNF
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Aah14793 Human cDN
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Adr14214 Human NF-
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Adr14038 Human cDN
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Ach89719 Human gen
Acn44177 Mouse gen
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ADS59288

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Aal39626 Human sec
Adq88659 Human tum
Adq86551 Human tum
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Adq86751 Human ip2
Abz11655 Human ip2
Abz11655 Human pol
Adm44173 Novel human
Aaf59594 Human gen
Aac10355 Human sec
Abl07183 Drosophil
Ach48309 Human im
Aac10359 Human cDN
Aah18715 Human cDN
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Aac165360 Rat micro
Ach78513 Human gen
Add76232 Cotton cD
Add76232 Cotton cD
Add99864 Human mus
Add76232 Cotton cD
Add87654 Mouse man
Acc14149 Mouse man
Acc14149 Human mus
Abc60109 cDNA encod
Add309864 Wheat ser
Abx91542 Modified
Abg87587 DNA encod
Aal17422 Human bre
Aac105596 Human tum
Adg81040 Human tum
Adg81040 Human tum
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Adg81040 Human sec
Add85040 Human sec
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Add12921 Human apa
Ach95566 Rat MURF1
Adc76232 Cotton cD
Aas64862 DNA encod
Add109351 Wheat ser
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Add513669 Human apa
Ach955866 Rat MURF1
Adc76234 Cotton cD
Aas64862 DNA encod
Add00898 Mouse hom
Add119351 Wheat ser
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Add119351 Whose hom
Add51940 Human apa
Ach95586 Human apa
Ach95966 Human apa
    Adj29706 Human mus
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Adk70980 Nucleotid
Adk70981 Nucleotid
Acm44584 Mouse gen
Adl03956 DNA encod
Abl28494 Drosophil
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                                                                                                                                                                                The invention relates to an anti-apoptopic gene SSC-S2 and encoded protein. The gene is a positive mediator of tumour growth and metastasis in certain cancer types. The SSC-S2 protein can be expressed by standard recombinant methodology. The SSC-S2 polypeptide is useful as a target for identifying compounds that modulate cancer progression by inhibiting apoptosis, as a target for detecting cancers where this polypeptide is overexpressed, e.g. renal and overian cancers, and leukemia. The antibody and antisense oligonucleotide can be used to treat cancer and to inhibit cancer cell proliferation and/or metastasis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New SCC-S2 polypeptides and nucleic acids encoding them, useful autarget for identifying compounds that modulate cancer progression inhibiting apoptosis, as a target for detecting cancers, or for
                                                                                                                                              Sequence 1915 BP; 610 A;
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
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                                 03-OCT-2001; 2001US-0327212P
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The invention relates to a novel method for identifying a compound that CC modulates T lymphocyte activation. The method comprises contacting a T CC cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound, CC where the A-raf- 1 or TCPTP/PTPN2 polypeptide is encoded by a nucleic acid that hybridises to a nucleic acid encoding a polypeptide having a CC sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has CC immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory CC activity. The method is useful for identifying compounds that modulate CC lymphocyte activation and migration, and for monitoring changes in cell Surface marker expression, cytokine production, antibody production, CC proliferation and differentiation, and apoptosis, using either cell lines CC corp rimary cells. The A-raf- 1 or TCPTP/PTPN2 proteins may be used as CC drug targets for compounds that suppress or activate lymphocyte activation and migration, e.g. for the treatment of diseases in which CC modulation of the immune response is desired such as delayed type and acute and chronic inflammation. Modulators of lymphocyte activation and care useful for treating disorders related T and B cell activation and CC invention.
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AAX97916 to AAX98029 represent 110 isolated human secreted protein genes. AAY36224 to AAX36727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or

Claim

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537pp;

English.

New isolated human genes encoding secreted polypeptides

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                                                                 cancer; inflammation; immune disorder; neurological disorder;
blood clotting disorder; food additive; food preservative;
storage capability; fat content; nutritional component; ds; gene;
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No. 1.4e-163;
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                                                                                                                                                                                                                                                                       The invention relates to an isolated HKABT24 nucleic acid molecule. The polypeptides, nucleic acids and antibodies are useful for diagnosing a complete pathological condition or a susceptibility to a pathological condition, for pathological condition, and the rimmune disorders, neurological and blood clotting disorders. The nucleic acids are also useful for chromosome clotting disorders. The nucleic acids are also useful for chromosome clotting in the polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues communological probes for differential identification of the tissues community of the sada as a food additive or preservative to contract of the protein. Note: The sequence represents convention of the printed specification but was obtained in electronic format directly from USPTO at the protein contract.
                                                                                                                                                                        Query Match
Best Local S
Matches 590
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Ferrie AM,
                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New secreted HKABT24 nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
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P-PSDB; ADA11694.
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18-DEC-1997;
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             TTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTAC
                                                        GCCGTTCANGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACC
                                                                      GCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACC
                                                                                                                 GTCCCGGCGCCGTCGCGCACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTG
TTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTTACAGAGTGACCAGGGAGTAC
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                                                                                                                                                                          Conservative
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97US-0068169P.
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97US-0068368P.
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New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or
                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding human secreted protein #420.
                                                                                                                                                    WPI; 2003-167512/16.
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neurodegenerative disorders

21; SEQ ID NO 430; 1754pp; English.

CC neurodegenerative disorders, or polypeptides comprising an amino acid compenses at least 95% identical to the new sequences. The polypeptides, antibodies or antibodies or antibody fragments that bind to the polypeptides, nucleic carids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune compositions for crohn's disease), respiratory disorders (e.g. asthma and callergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative (e.g. atherosclerosis or myocarditis). The controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identification, chromosome comminute biological samples, in forensic biology, and as hybridization or antisense DNA or RNA, in gene therapy, for identifying individuals comminute biological samples, in forensic biology, and as hybridization controlling neural disorders (e.g. els, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, creating or preventing neural disorders, immune system disorders, and for the sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at The invention relates to 592 new human secreted polypeptides useful fo diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or ftp.wipo.int/pub/published_pct_sequences

Sequence 1943 BP; 629 A; 325 C; 399 G; 586 T; 0 U; 4 Other;

Matches 590; Query Match Best Local Similarity 97.9**%**; 99.3**%**; <u>,</u> Score 588.2; DB 10 Pred. No. 1.4e-163; Mismatches DB 10; Length 1943; 0 Gaps 0

Qy	8 GTCCCGGCGGCCGTCGCCCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTTG 67	
Вb	93 GTCCCGGCGCGTCGCGCACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAAACCTG 152	
Qy	68 GCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACC 127	
ДЪ	153 GCCGTTCANGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACC 212	
Qy	128 TTAATAGACGACACAAGTAGTGAGGGGGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTAC 187	
Ъ	213 TTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCCAGGGAGTAC 272	
γ	188 ACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAG 247	
ф	273 ACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAG 332	
Qy	248 CTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGAGAAA 307	
Вb	333 CTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAA 392	
γQ	-1	
Вb	393 TTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTAT 452	
Qγ	368 ACCTTTGACCGGAATGTGTTATCCAGGCTGTTAAATGAATG	
ф	453 ACCTTTGACCGGAATGTGTTATCCAGGCTGTTAAATGAATG	
δ	428 ATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCAT 487	
망	513 ATCATTCAGCGCCACTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTTGATCAT 572	
Ş	488 TTTTCAGATTGTGAATTTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTTAAACCCCAC 547	

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RESULT 6
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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, Sugiyama
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; 2000JP-00183767.
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Best Local Similarity
Matches 599; Conser
29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
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99JP-00300253.
2000JP-00118776.
2000JP-00183767.
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                                                                        99JP-00248036.
                                                                                                                                                                                                                                                                                                                              detection;
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                                                                                                                                                                                                                                                                                                                              diagnosis; antisense therapy; gene therapy;
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Pred. No. 3.6e
0; Mismatches
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Matches 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03165 to AAH13628 and callsonucleotides, all of which are used in the exemplification of the oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1729 BP;
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.. Sugiyama T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
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                                                                                                                                                                                                                                                                                                                                 TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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                             TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                                   TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTTGACCGGAATGTGTTTATCCAGGC
                                                                                                                                                                                                                                                    TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTA
                                                                                                                                                                                                                                                                                                    TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                     TGACCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                          TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGA
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defined in the specification. Where a primer set comprises:
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Pred. No. 1.5e-156;
0; Mismatches 1;
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A, Nagai K,
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Otsuki
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This invention relates to the novel association of protein sequences the genes which encode them) to the NF-kappaB pathway. The invention be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides useful for diagnosing, preventing, treating, or ameliorating conditio

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                                                                                                                                                                                                                                                                                                        New isolated polynucleotides and polypeptides associated with pathway, useful for diagnosing, treating, or preventing disord diseases associated with NF-kappaB pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer; HIV propagation; gene; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disorder; NF-kappaB regulation; cancer; aberrant apop hapatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HTV-1; HTLV-1; hepatitis B; hapatitis C; EBV; inf viral replication; host cell survival; evasion of immune response; rheumatoid arrhritis; inflammatory bowel disease; colitis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiatthritic; antirheumatic; gastrointestinal-Gen; antiathmatic; antirheumatic; crebbroprotective; vasotropic; antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic; immunosuppressive; vulnerary; gene therapy; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nadler SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2003; 2003US-0440068P.
12-MAY-2003; 2003US-0469757P.
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DB; ADR14215.
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                                                                                                                                                                                                                                                              215;
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                                                                                                                                                                                                                                                        237pp; English.
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immune disorder, an inflammatory disorder, an inflammatory disorder related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, thepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, with infections, HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral infections, hiv-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant correction, disorders related to aberrant signal transduction, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.
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Best Local S
Matches 565
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                                                                                                                                                                                                                         CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                                                                                                                                                                                                                            TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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AAATGTTGGATGAAGAGAACATATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
                                                                                                                                 TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                                                                         CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                                                                                                                                                                                     TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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Pred. No. 1.6e-156;
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                    601
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immunosuppressive; vulnerary; gene therapy; immune disorder; inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; x-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HTV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer;
Nadler SG,
                                                                                                                                                               14-JAN-2003; 2003US-0440068P
12-MAY-2003; 2003US-0469757P
                                                                                                                                                                                                                                                                                    13-JAN-2004; 2004WO-US000798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV propagation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarthritic; antirheumatic;
                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
Neubauer MG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ds; human.
    Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal-Gen; antiasthmatic
        Carman
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New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.

Claim 1; SEQ ID NO 217; 237pp; English.

CC vulnerary activity or for gene therapy. The proteins and nucleotides are cuseful for diagnosing, preventing, treating, or ameliorating conditions conditions diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder an inflammatory disorder related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, concertaint disorders, Hodgkin's lymphomas, haematopoletic tumours, hyper-IgM comparities by hypohidrotic ectodermal dysplasia, X-linked anhidrotic concorderations, himmunodeficiency, viral infections, HTV-1, HTV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell convival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper congenital conditions, birth defects, necrocic lesions, wounds, corgan transplant rejection, conditions related to organ transplant corporation, disorders related to aberrant signal transduction, disorders related to aberrant signal transduction, disorders related to aberrant signal transduction, for the present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the subject to the novel association with the NF-kappaB pathway invention. Note: This sequence does not appear in the specified was obtained by the indexer from Genbank. be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, gastrointestinal-den, antiasthmatic, antiarteriosclerotic, immunosmodulator, cerebroprotective, vasotropic, immunosuppressive o This invention relates to the novel association of protein sequences the genes which encode them) to the NF-kappaB pathway. The invention

ADR14216 ID ADR1 XX AC ADR1 XX

ADR14216 standard; DNA; 2003

ВP

ADR14216;

RESULT 9

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RESULT 10
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ID ACN44
XX ACN44
XX 18-NO
DT 18-NO
XX Cytos
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XX Homo
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PN WO200
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Best Local Similarity
Matches 565; Conserv
                                                                                                                                                                                                Human mRNA
 Morris
                                                                                                                        WO2003073826-A2
                                                                                                                                                                     Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                         18-NOV-2004
                                                                                                                                                                                                                                                  ACN44179
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                         (SAGR-) SAGRES DISCOVERY
                                               01-MAR-2002; 2002US-00087192
                                                                       28-FEB-2003; 2003WO-US006235
                                                                                                 12-SEP-2003
                                                                                                                                                                                                                                                                         ACN44179 standard; cDNA;
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ilarity 99.8%;
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Recombinant nucleic acid useful for diagnosis and treatment comprises a nucleotide sequence.
                                                                                          2003-328604/31
                                                                                  엵
                                                                                  carcinoma
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SEQ ID

NO 497; Opp; English.

The present invention relates to novel DNA and protein sequences which CC are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) as a biochip; (c) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma or a propensity to carcinoma; and (xi) for considerated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This patent is an equivalent to basic patent useful as markers of useful as markers of the copy number.

Sequence 2034 BP; 639 A; 352 C; 412 G; 631 T; 0 U; 0 Other;

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Query Match
Best Local S
Matches 565
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                  AAATGTTGGATGAAGAGAACATATGA
                                                                                TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                             CACATGGACGGGTTAATAATGTGTTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
                                                                                                                                                                                              TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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Pred. No. 1.7e-156;
0; Mismatches 1;
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814
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RESULT 11 ADR14038 ID ADR14

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ADR14038 standard; DNA; 2081 ВP

ADR14038;

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CC This invention relates to the novel association of protein sequences (and CC the genes which encode them) to the NF-kappaB pathway. The invention may CC be useful for the production of compounds with an antiinflammatory, CC cytostatic, hepatotropic, virucide, antiarthritic, antiinfumatic, CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic.

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or cytostatid for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder crelated to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypehidrotic ectodermal dysplasia, X-linked anhidrotic cetodermal dysplasia, immunodeficiency, viral infections, HVV-1, HTLV-1, CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper congenital conditions, birth defects, necrocic lesions, wounds, crejection, disorders related to aberrant acute phase responses, cuthfor disorders related to aberrant signal transduction, fielded control of the virees free and HIV propagation in cells infected with other virees free and HIV propagation in cells infected with the process and HIV propagation in cells infected with the process and HIV propagation in cells infected with the process and HIV propagation in cells infected with the process and HIV propagation in cells infected with the process and HIV propagation in cells infected with the process and HIV propagation in cells infected with the process and HIV propagation in cells infected with the process and HIV propagation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 39; 237pp; English.
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12-MAY-2003; 2003US-0469757P.
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The present sequence
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     propagation in cells infected is that of a human gene which
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Best Local Similarity
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                 AAATGTTGGATGAAGAGAACATATGA
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                                                                              TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                       CACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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AAATGTTGGATGAAGAGAACATATGA
                                                           TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                         CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
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99.8%;
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Pred. No. 1.7e-156;
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ACN44178
ID ACN44
XX ACN44
AC ACN44
XX 18-NO
DT 18-NO
DE Human
XX Cytos
XX Homo
OS Homo
XX WO200
PN WO200
XX 12-SE
PF 28-FE
XX X
           01-MAR-2002; 2002US-00087192
                                                                                                                 Cytostatic; carcinoma; lymphoma; cancer; human;
                                                                                                                                       Human genomic sequence hCG36837
                                                                                                                                                             18-NOV-2004
                                                                                                                                                                                  ACN44178;
                                                                                                                                                                                                      ACN44178 standard;
                               28-FEB-2003; 2003WO-US006235.
                                                                        WO2003073826-A2
                                                                                            Homo sapiens
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bloactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for a carcinoma; (vi) for inhibiting the activity of CAP; (v) for diagnosing carcinoma; (vi) for neutralizing the activity of CAP; (vi) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a blochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586AI, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
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                                                                                                                                                CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTTGTGAATTTTTTGGCTGCCT
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AAATGTTGGATGAAGAGAACATATGA 47503
                   AAATGTTGGATGAAGAGAACATATGA
                                                                                       TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                                                                               TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                                                                                                                                                                TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid useful for diagnosis and treatment of nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to novel DNA and protein sequences which ted with carcinomas. The sequences are useful for: (i) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16891 A; 11477 C; 12539 G; 17816 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.9%;
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Pred. No. 8.
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TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG

161 95

102

Query Match Best Local S Matches 562

Similarity

91.1**%**; 98.9**%**; A; 155

Score 547.6; Pred. No. 1e-1 0; Mismatches

547.6; DB 4; No. 1e-151;

816; 2;

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CC length cDNAs defined in the specification. Where a primer set comprises:

(C (a) an oligo-dT primer and an oligonucleotide which comprises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 cc complementary strand of a polynucleotide which comprises one of the 5602 cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination co of an oligonucleotide comprising a sequence complementary to the cc complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the cc oligonucleotide which comprises and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in c specification. The primer sets can be used in antisense therapy and in c sparticularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the combination of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and constraint of the combination of the comprises allow obtaining of the AAH3628 and constraint invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 ful length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2537pp + Sequence Listing; English
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A, Nagai K,
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C, Otsuki
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                                             New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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Query Match
Best Local (
    Sequence 544 BP; 175 A; 109 C; 117 G; 143 T; 0 U; 0 Other;
                                                               Claim 1; SEQ ID NO 22914; 80pp; English
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Matches 543; 301 181 361 396 241 121 456 156 61 36 96 GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT TGTTAAATGAATGCAGAGAGAGATGCTGCCAAATCATTCAGCGCCCACCTCACTGCCAAGT TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA TTAATCAAGATGAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA GTAAAATGGTGTCCAAATCCATCGCCACCATCATAGTAGACGACACAAGTAGTGAGGTGC TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG Conservative 0; Mismatches es 1; Indels 0; Gaps 515 300 335 180 215 155 420 455 360 395 240 275 120 60

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Local Similarity

90.2%;

Score 542.4; DB 12; Pred. No. 2.9e-150;

Length

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                                                                                                                                                                                                       The present invention relates to novel DNA and protein sequences which care associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (iv) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating (carcinoma; (viii) for neutralizing the effect of CAP; (vii) for the capable of carcinoma; (viii) for neutralizing the effect of CAP; (vii) as a biochip; (vx) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining carcinoma or a propensity to carcinoma; and (xi) for carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent (vx) US2002182586A1, for which no sequence data was published
                                                                                                                     Query Match
Best Local S
Matches 494
                                                                                                                                                                                Sequence
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                   GATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCTTAATAGACGACGACACAAGTAG
                                                                              TCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAA
                                                                                                                                                                               62231 BP; 15482 A; 12591 C; 12729 G; 16514 T; 0 U;
                                                          TTCTGCAGTGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAA
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RESULT 16
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
                                                                                                                                  Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                     Claim 1; SEQ ID NO 494; Opp; English.
                                                                                                                                                                                                                                                                  01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                                                              12-SEP-2003
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RESULT 1:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2087 BP; 556 A; 487 C; 508 G; 536 T; 0 U; 0 Other;
   07-FEB-2001
                                  EP1074617-A2
                                                                                                Human; primer;
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                                                                                                                                 cDNA clone (5'-primer) SEQ ID NO:4476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAGAAGATCTTGG
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                                                                                               detection; diagnosis; antisense therapy; gene therapy;
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Pred. No. 6.8e-121;
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clength cDNAs defined in the specification. Where a primer set comprises:
cc (a) an oligo-dT primer and noligonucleotide complementary to the
cc complementary strand of a polynucleotide which comprises one of the 5602
cn uncleotide sequences defined in the specification, where the
cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination
cc of an oligonucleotide comprising a sequence complementary to the
cc complementary strand of a polynucleotide which comprises a 5'-end
cc sequence and an oligonucleotide comprising a sequence complementary to a
cc polynucleotide which comprises a 1'-end sequence, where the
cc polynucleotide which comprises a 1'-end sequence of the 5'-end sequence/3'-end sequence is selected from those defined in the
cc plication. The primer sets can be used in antisense therapy and in
cc particularly full-length cDNAs. The primers are also useful for the
cc gene therapy. The primers have been antisense therapy and in
cc particularly without any specialised methods. AAH03166 to AAH13628 and
cc cDNAs easily without any specialised methods. AAH03166 to AAH13632 represent
cc paresent human amino acid sequences; and AAH13629 to AAH13632 represent
corresent invention
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Best Local S
Matches 422
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 fullength cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
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Sugiyama
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                                                                                          GGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                                           CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                  587
                                                                                                                                                                                                                                                                               CTTCAGCGTCCCGGCGCCGTCGCGCCACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                                                                                                                                                                                                                                                                CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTAATTCCA 59
                                                                                                                                         CCACCACCTTAATAGACGACACGAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                                                                                             AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTGCCAAATCCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO
TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
                     TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
                                                                     GGGAGTACACCCAAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                                                                                             AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                 A; 146 C; 140 G; 116 T; 0 U; 7 Other;
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Pred. No. 2.2e-106;
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C, Otsuki
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TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG

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                                                                                                                                  Query Match
Best Local S
Matches 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T, S
Yamamoto J,
                                                                                                                                                                                                                                                                              The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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DB; ADQ65296.
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                                                            150
                                                                                                 42
                                                                                                                                                     Similarity
TGGTGTCCAAATCCATCGCCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATG
                                                                                                                                                                                                                                               and various cancers. of the invention.
                                                                               CAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAA
                                                                                                                                                                                                            1986
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID
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                                                          CTGATGTTTTTAGTTCAAAGAGTCTTGCGCTTCAAGCCCAGAAGAAGATTCTGAGCAAAA
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J, Isono Y,
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                                                                                                                                      Conservative
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Nagai K,
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0; Mismatches
                                                                                                                                                   Score 254.4;
Pred. No. 1.
                                                                                                                                                                                                      C; 497
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Zhou P, Ghosh M
Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                                         ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's diseaseneurodegenerative diseases; anaemia; platelet disorder; wound;
                                                                                                                                                                                    24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                         24-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
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                                                                                                                                                                                                                                                              10-APR-2003
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                     2003-371981/35
DB; ADC31740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel cDNA sequence, SEQ ID NO:851.
                                                                                         Zhang J,
Ghosh M,
                                                                                                                                                 HYSEQ INC
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Asundi
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Wehrman ç

nootropic; cytostatic;

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CC ADC3089) and the polypeptides they encode (ADC30890-ADC3080). The clivention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression convectors and host cells comprising a nucleic acid of the invention; the crecombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting polynucleotides or polypeptides of the invention; and methods of compound which binds to a polypeptide of the invention. The cinvention further discloses methods of peventing, treating or ameliorating a medical condition; kits compounds that modulate the cinvention; methods for the identification of compounds that modulate the contract sequences corresponding to the cDNA sequences of the invention are conting sequences corresponding to the cDNA sequences of the invention are identification of mucleic acids and polypeptides of the invention are constituted acids and polypeptides of the invention are constituted for treating biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are caused for treating diseases such as Parkinson's disease, Alzheimer's cdisease and other neurodegenerative diseases, anaemia, platelet consers, and in the recombinant production of a protent. The polypeptides or cancer. The nucleic acids may also be used as hybridisation probes or concers, and in the recombinant production of a protent. The polypeptides care also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically collaboration and electronic format directly from WIPO at the sequence data for this patent did not form part of the printed specification, but was considered to the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 969 BP; 264 A; 261 C; 257 G; 187 T; 0 U; 0 Other
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ATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATG
                                                                                                                        TGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGTTAA
                                                                                                                                                                                                                     AAGAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCA
                                                                                                                                                                                                                                                                      AAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCG
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                                                                       TTGTCAGCTTCTATGAGGTGGAATACACCTTCGATAGGAACGTGCTCTCCAATCTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 2.6
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide concludes in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon mucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PENN/) PENN S G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human genome-derived single exon nucleic acid probes useful for gene expression analysis, for identifying or characterizing alternate splicing events, for assessing genomic alterations or as tools for
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Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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31-OCT-2001;
04-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; inferrility; inflammatory bowel disease; atherosclerosis; hypertension; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parasitic infection; graft-versus-host disease; cell differentiation; cell proliferation; haematopoiesis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell differentiation; c angiogenesis; gene; ds.
                                                                                                                                                                                                                                                                                               Spytek KA,
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13-MAR-2001;
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                                                                                                                                                                                                                                                                                                                    (CURA-)
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Zerhusen BD, Patturajan M, Gusev
M, Gangolli EA, Taupier RJ;
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                                                                                                                                                                                                                                                                                                                    CORP.
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                                                                                                                                                                                                                                                                                       Kekuda
                                                                                                                                                                                                                                                                                                Gerlach VL;
                                                                                                                                                                                                                                                                                      ₽,
                                                                                                                                                                                                                                                                                       Pena CEA;
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New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or Zhong WPI; 2002-713508/77. P-PSDB; ABG97497. Σ, multiple

Claim 22; Page 139; 266pp; English.

Parkinson's disease.

The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, erebral pylopercalcaemia, Parkinson's disease, Huntington's disease, cerebral pylopercalcaemia, Parkinson's disease, Huntington's disease, cerebral pylopercalcaemia, Parkinson's disease, multiple sclerosis, ataxia-telangicctasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, crohn's disease, osteoporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, panoreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, wound healing and parasitic

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RESULT 2:
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               antiasthmatic; cardiant; vasotropic; neuroprotective; nootropic; SECP; anticonvulsant; antiparkinsonlan; cerebroprotective; antiinflammatory; immunosuppressive; human secreted protein; cell proliferative disorder; arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; allergy; anaemia; asthma; cardiovascular disease; developmental disorder; ischaemic heart disease; congestive heart failure; neurological disorder; renal tubular acidosis; hypothyroidism; Albelmer's disease; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and probes, in chromosome mapping, tissue typing, preventive medicine, and probes, in chromosome mapping, tissue typing, preventive medicine, and probes, in chromosome mapping, tissue typing, preventive medicine, and probes, in chromosome mapping, tissue typing, preventive medicine, and probes, in chromosome mapping, the present nucleic acid sequence encodes a human NOVI pharmacogenomics. The present nucleic acid sequence encodes a human NOVI pharmacogenomics.
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                                                                                                                                                                     뭐
                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated human secreted protein (SECP)

CD polypeptide from 63 fully defined protein sequences given in the

CD polypeptide from 63 fully defined protein sequences given in the

CD specification. The polypeptide is useful for the diagnosing/treating of a

CD disease with decreased/overexpression of SECP. Examples of disorders

CD associated with abnormal expression of SECP include a cell proliferative

CD disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory

CD disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g.

CD congestive heart failure, ischaemic heart disease; developmental disorder

CD congestive heart failure, ischaemic heart disease; developmental disorder

CD congestive heart failure, ischaemic heart disease; gellepsy or stroke.

CD Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke.

CD CD creating knockin humanised and polypeptide are further useful for analysing

CD creating knockin humanised animals (pigs) or transgenic animals (mice or

CD creating knockin human disease, and for somatic or germline gene therapy,

CD conditions of the invention

CD creating dementing phybridisation probes useful in mapping the

CD creating cocurring genomic sequence. This polymucleotide sequence

CD creating the bulk of a human secreted protein of the invention
                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000;
09-NOV-2000;
16-NOV-2000;
21-NOV-2000;
08-DEC-2000;
18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yue H, Yao MG, Gandhi
Sanjanwala M, Thornton
Ding L, Hafalia AJA, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing
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      203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted proteins and polynucleotides nting disorders of cell proliferative, opmental, neurological and autoimmune/i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                       83
                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                    Similarity
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GAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTAT
                                         AGCAGTGAGGTGCTGGATGAGCTGTACCGCGCCACCAGGGAGTTCACGCGCAGCCGCAAG
                                                            AGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCCAAAAACAAGAAG
                                                                                                       AAGAAGCTCCTGAGTAAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGATGACACC
                                                                                                                                      CTGTGTCCCCCGCAGGCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAGGCGCAG
                                                                                                                                                                                                     CCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thangavelu K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duggan BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0247505P.
; 2000US-0248642P.
; 2000US-0249824P.
; 2000US-0252824P.
; 2000US-0254305P.
; 2000US-0256448P.
                                                                                                                                                                                                                                   34.6%;
ilarity 59.9%;
Conservative
                                                                                                                                                                                                                                                                                                   BP;
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                                                                                                                                                                                                                                                                                                   408 A;
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Sapperstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĭ AR
                                                                                                                                                                                                                                                                                                      602
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Elliott VS,
g YT, Bandman o
e S, Xu Y, Ya
erstein SK;
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                   Score 207.8; DB 6
Pred. No. 1.1e-50;
0; Mismatches 232
                                                                                                                                                                                                                                                                                                     C; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ynucleotides for diagnosing, oliferative, cardiovascular, autoimmune/inflammatory disc
                                                                                                                                                                                                                                                                                                   G;
                                                                                                                                                                                                                                                                                                     462
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Lu Y, Gietzen KJ, Burfo
O, Warren BA, Honchell
and J, Lal PG, Tran B;
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                                                                                                                                                                                                                                       Gaps
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GAGGCCCAGAAGATGCTCAAGAACCTGGTCAAGGTGGCCCTGAAGCTGGGACTGCTGCTG

651

591 202 531 471

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RESULT 23
ADQ85659
The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID No:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence
                                                                                                                                                                                                                                                             New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2473; 5504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004060270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2002; 2002US-0418988P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-2003; 2003WO-US029126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ85659 standard; cDNA; 2186 BP
                                                                                                                                                                                                                                                                                                                                                                                                    (ZHOU/)
                                                                                                                                                                                                                                                                                                                           2004-534300/51
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) WU T D.
) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour-associated antigenic target; TAT; cytostatic; gene therapy;
; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                              Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCAC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGGCCTGGGATGCTGGACGAGGGCAGCCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAAT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTGGGGACCAGCTGGGCGTGAGGAGCTGGCGGCGCTGCGGCGCGCTTCCGCCACCGGGCG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTGGCTGCGCTACGGCCCCGAGCCCTACCGCTCCCACCTGCGCAGGATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGT 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGACCGCCAAGTCCCACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGACTGCGAC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTGGCCGGGCTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCTGCCTGGCCATGACGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence #2473.
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                                              CC comprising the above polypeptide fused to a heterologous polypeptide; (6) cc an isolated antibody that binds to the above polypeptide; (7) a process cc for producing the antibody; (8) an isolated oligopeptide; (7) a process cc for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (10) a cc composition of matter comprising the above (chimeric) polypeptide, (10) a cc composition of matter comprising the above polypeptide, in combination composition of matter comprising the above (chimeric) polypeptide, (10) a composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of cinhibiting the growth of a cell that expresses the above protein, where cc the growth of the cell is at least in part dependent upon a growth cc inhibiting effect of the above protein; (13) a method of cells that express the above protein; (13) a method of determining the protein in a sample suspected of containing the protein cells that express the above protein; (14) a method of described above; (15) methods of diagnosing the presence of a protein in a sample suspected of containing the protein companic malecule to a cell that expresses the above protein; (13) a method of containing the protein corganic melecule to a cell that expresses the protein described above. Cc protein, and (17) a method of binding an antibody, oligopeptide or corganic melecule to a cell that expresses the protein described above. Cc the TAT sequences have cytostatic activities, and can be used in gene cc therapy. The composition and methods are useful for diagnosing, cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative dis
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2186 BP; 478 A; 624 C; 673 G; 411 T; 0 U; 0 Other;

Matches Query Match Best Local

347;

h 34.0%; Similarity 59.3%; 47; Conservative

<u>,</u>

Score 204.2; DB 12; Pred. No. 1.3e-49; 0; Mismatches 238;

238; Indels

0;

Gaps

0

Length 2186

片 δ 밁 Ş Ś S á 밁 В 밁 밁 Ś 밁 497 512 437 377 452 137 152 77 92 CGGACTCTGCTTCGAGAGTAGGCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAG 17 AAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATT AAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGAC ATCTGCGAGGCCTGGGCCGGATGCTGGACGAGGGCAGCCTCTGA 676 CTATGTGATGGTATCAACAAATGTTGGATGAAGAGAACATATGA TGCGACTTCCTGGCTGCGCTCTACGGCCCCGCCGAGCCCTACCGCTCCCACCTGCGCAGG TGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAA 556 CCCCACCTGACCGCCAAGTCCCACGGCCGCATCAACCACGTGTT CGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGAT CGGCGCGTGCTGGCCGGGCTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGT CGGAATGTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAG CGGGCGCGCTGCCTGGCCATGACGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGAC CTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAG CGCAAGGAGGCCCAGAAGATGCTCAAGAACCTGGTCAAGGTGGCCCCTGAAGCTGGGACTG GACACCAGCAGTGAGGTGCTGGATGAGCTGTACCGCGCCACCAGGGAGTTCACGCGCAGC GACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAC GCGCAGAAGAAGCTCCTGAGTAAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGAT GCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGAC ccercecceacrecceares en a contrata contrata en a contrata CTGCTGCGTGGGGACCAGCTGGGCGGTGAGGAGCTGGCGCCTGCTGCGGCGCTTCCGCCAC 601 571 496 436 391 331 256 271 196 211 136 151 76 451

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ADQ86751
ADQ86752
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                  CC sequences (see SEQ IN NO:1 to 46221; (b) the full-length coding region of CC (a); (c) the complement of (a) or (b) (d) a sequence that has 80% CC (c). Also described: (1) an expression vector comprising the above mucleic acid; (2) a host cell comprising the above expression vector; (3) CC a process for producing a polypeptide; (4) an isolated polypeptide CC comprising; (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-CC length coding region of the above nucleotide sequences; (c) a sequence cC chaving at least 80% identical to (a) or (b); (5) a chimeric polypeptide; (6) CC an isolated antibody that binds to the above polypeptide; (6) an isolated antibody that binds to the above polypeptide; (6) an isolated oligopeptide that binds to the above polypeptide; (6) antibody, oligopeptide; (9) a tumour-associated antigenic target (7MT) CC binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (6) antibody, oligopeptide or TAT binding organic molecule, in combination CC with a carrier; (11) an article of manufacture comprising a container and CC inhibiting the growth of a cell that expresses the above protein, where CC inhibiting the growth of a cell that expresses the above protein, where CC inhibiting the protein in a sample suspected of containing the protein of cells that expresses the above protein of cells that expresses the above protein and cell proliferative container; (12) a method of containing the protein and container and cell that expresses the above protein and containing the protein and container and cell that expresses the protein determining the composition and cell that expresses the protein determining the protein and container and cell that expresses the protein determining the composition and methods of disorder associated with increased expresses the protein described above. The composition and cell be a cell that expresses the protein descr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3626; 5504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
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   preventing or
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) WU T D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes an isolated tumour-associated and nucleic acid comprising: (a) any of 4622 nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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       cancer.
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The composition is also
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2186 BP; 478 A; 624 C; 673 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human TAT cDNA sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents
632
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                                                                                                                                                                                                                                                                                                                                                                                                AAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATT
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ATCTGCGAGGCCTGGGCCGGATGCTGGACGAGGGCAGCCTCTGA 676
                             CTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA
                                                                                                                        CCCCACCTGACCGCCAAGTCCCACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGAC
                                                                                                                                               CGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGAT
                                                                                                                                                                                      CGGCGCGTGCTGGCCGGGCTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGT
                                                                                                                                                                                                                                                  CGGGCGCGCTGCCTGGCCATGACGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGAC
                                                                                                                                                                                                                                                                                 AAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGAC
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                                                             TGCGACTTCCTGGCTGCGCTCTACGGCCCCGCCGAGCCCTACCGCTCCCACCTGCGCAGG
                                                                                         TGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAA
                                                                                                                                                                                                             CGGAATGTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAG
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Pred. No. 1.3
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ADQ84271 standard;
18-OCT-2002; 2002US-0418988P
                                                                                   human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene;
                                                                                                            Human tumour-associated antigenic target (TAT)
                                                                                                                              07-OCT-2004
                                                                                                                                               ADQ84271;
               15-OCT-2003; 2003WO-US029126
                                  22-JUL-2004
                                                  WO2004060270-A2
                                                                   Homo sapiens
                                                                                                                              (first entry
                                                                                                                                                               cDNA; 2186
                                                                                                                                                                Β₽
                                                                                    TAT;
                                                                                                            cDNA sequence
                                                                                           cytostatic; gene therapy;
                                                                                                             #1085
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The present invention describes an isolated tumour-associated antigenic (arrayet (TAT) nucleic acid comprising: (a) any of 4622 nuclectide (CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequences (see SEQ IN NO: to 4622; (b) the full-length coding region of (CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(CC (c) Also described; (l) an expression vector comprising the above mucleic acid; (2) a host cell comprising the above expression vector; (3) (CC a process for producing a polypeptide; (4) an isolated polypeptide (CC comprising: (a) an amino acid sequence encoded by any of the above comprising the above polypeptide; (b) an amino acid sequence encoded by the full-(CC length coding region of the above nucleotide sequences; or (c) a sequence (CC comprising the above polypeptide; (f) an isolated antibody; (a) an isolated oligopeptide; (f) a process (c) an isolated antibody; (a) an isolated altipenic target (TAT) (CC binding organic molecule that binds to the above polypeptide; (l) a process (c) a sequence (c) antibody; (l) an article of manufacture comprising a container and the composition of matter comprising the above (chimeric) polypeptide; (l) a composition of matter comprising the above (chimeric) polypeptide; (l) an isolated altipenic target (TAT) (CC binding organic molecule; in combination (c) inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth of the cell is at least in part dependent upon a growth (c) the growth of the above protein; (l1) a method of determining the protein in a sample suspected of containing the protein (c) presence of a protein in a sample suspected of containing the protein (c) and colored above (c) a method of determining the protein (c) and colored above (c) and colored a
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-534300/51
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347; Conserv
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                                                                                                                                                                        GCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCCTTAATAGAC
AAGAAGGAGGAGAGAAGATCAATGAAGACCTCATCAAGACAGTCATCAAGCTGGCCATT
                                                                                                  GACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGGAGTACACCCCAAAAC
                                                                                                                                                                                                                                                               CCGTCGCCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTTGGCCGTTCAG
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                                                               GACACCAGCAGTGAGGTGCTGGATGAGCTGTACCGCGCCACCAGGGAGTTCACGCGCAGC
                                                                                                                                                GCGCAGAAGAAGCTCCTGAGTAAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGAT
                                                                                                                                                                                                                               CGGACTCTGCTTCGAGAGTAGGCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAG
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                  Score 204.2; DB 13; Length Pred. No. 1.3e-49; Indels 0; Mismatches 238; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                   G; 411 T; 0 U;
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                 08-MAR-2001;
09-MAR-2001;
12-MAR-2001;
13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
20-MAR-2001;
20-MAR-2001;
21-MAR-2001;
21-MAR-2001;
22-MAR-2001;
23-MAR-2001;
23-MAR-2001;
27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; Von Hippel-Lindau Syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain; obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; atherosclerosis; hypertension; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parastic infection; graft-versus-host disease; cell differentiation, cell proliferation; haematopoiesis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGAATGTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGAC
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; 2001US-0274281P.

2001US-0275235P.

2001US-0275579P.

2001US-0275601P.

2001US-0277337P.

2001US-0277337P.

2001US-027733P.

2001US-027733P.

2001US-027733P.

2001US-027733P.

2001US-027783P.

2001US-027783P.

2001US-0277834P.

2001US-0278452P.

2001US-0278452P.

2001US-0279036P.

2001US-0279036P.
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02-APR-2001; 2001US-028802P.
02-MAY-2001; 2001US-0288148P.
31-MAY-2001; 2001US-0294821P.
31-CCT-2001; 2001US-03333075P.
04-DEC-2001; 2001US-0333375P.
07-MAR-2002; 2002US-00094466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haemopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probles, in chromosome manning times.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxiatelangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, inferrility, inflammatory bowel disease, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asterial and the content of the conte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmacogenomics. The proprotein of the invention
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d, Gangolli EA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURAGEN CORP.
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                                                                                GCTCAAGAACCTGGTCAAGGTGGCCCCTGAAGCTGGGACTGCTGCTGCGTGGGGACCAGCT
                                                                                                                                CATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTATAGGAATAATCAGTT
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Pred. No. 1.
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usev VY, Kekuda
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nes 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection, bacterial infection; fungal infection; diabetes; asthm autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.
            The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal and disorders such as viral infections, bacterial infections, fungal
                                                                                                                                                                                   Five hundred and ninety two polynucleotides derived from human tissue sources which encode secreted proteins, use: immune deficiencies and disorders such as autoimmune disorders.
                                                                                                                                                       Claim
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                                                                                                                                                                                     from a variety of useful for treating disorders.
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Best Local (
                              Human; secreted protein; atherosclerosis; Alzheimer's disease; LP237; diabetic retinopathy; severe combined immunodeficiency; pancreatitis; rheumatoid arthritis; colorectal adenoma; haemolytic anamia; cancer; reperfusion injury; arteriosclerosis; wound healing; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerrative diseases (e.g. Alzheimer's disease, parkinson's disease, liver fibrosis, coagulation disorders (e.g. haemophilia),
                                                                                                                                                                                                                                          AAD38699
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                                                                                                                          secreted protein encoding cDNA.
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Pred. No. 3.6e-43;
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                   psoriasis;
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                                                                                                                                                                                                                                                                                                                                                      The invention relates to human secreted polypeptides designated LP095, LP219, LP217, LP220, LP221, LP222, LP229, LP237 or LP338 and nucleic acid molecules encoding such polypeptides. Novel secreted proteins of the invention are used for treating diseases such as atherosclerosis, attractionare disease, diabetic retinopathy, psoriasis, pancreatitis, attraction industrial attraction are used immunodeficiency, ischaemia, carcinomas, haemolytic anaemia, combined immunodeficiency, ischaemia, carcinomas, haemolytic anaemia, reperfusion injury, neoplasms and cancer especially liver cancer. They are also used for wound healing. Polymucleotides of the invention can be used to generate transgenic animals or knock out animals, which in turn, are useful in the development and screening of therapeutically useful reagents for use in the treatment of diseases associated with LP polypeptide associated activity. They are also used in gene therapy. The present sequence is human LP237 secreted protein encoding cDNA
                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel proteins and polynucleotides of secreted proteins useful for treating various diseases e.g. rheumatoid arthritis, cancer, psoriasis, diabetic retinopathy, arteriosclerosis, ischemia or reperfusion injury.
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                                                                                                                                                                                                                                                                                                                                                      Sequence 1165 BP;
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                                                                          AGAAGAT CATCAAGAACCT CATCAAGACAGT CATCAAGCTGGCCATTCTTTATAGGAATA
                                                                                                        AGGTGCTAGATGAGCTCTACCGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCC
                                                                                                                           AGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGGCAG
                                                                                                                                                                   TACTGAGTAAGATGGCGGGTCGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTG
                                                                                                                                                                                       TCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTG
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                                             AGCGCGTGATCAAGGACCTGATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATG
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1.7e-43;
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  The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The
protein or complementary secidentifying expressed genes
                                                                                                                                                                                              New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                          Claim
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DB; ABP69438.
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T, Wang
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Ma Y, Yamazaki V, Chen
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disorder

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cancer;

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03-JUN-2004 ADM44173; ADM44173

(first

entry)

standard;

cDNA; 1175

human arginine-rich protein cDNA

Homo sapiens

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Query Match
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Pred. No. 3.7e-43;
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05-MAR-2002;
20-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/c treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-238579/22.
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DRMANAC R
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CCAAGTCACATGGCCGCATCCGCCACGTGTTTGATCACTTCTCTGACCCAGGTCTGCTCA
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; 2002WO-US005095.
; 2002US-00225251.
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Pred. No. 3.7e-43;
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CC Sequences AAF59590-AAF59643 represent cDNAs encoding 54 human cell cycle CC and proliferation proteins (CCYPR), AAB60453-AAB60506. CCYPR and agonists CC of CCYPR are used to treat diseases or conditions associated with cc decreased expression of functional CCYPR, while CCYPR antagonists are CC used to treat diseases or conditions associated with overexpression of functional CCYPR, while CCYPR antagonists are CC used in enzyme-linked immunosorbent associated with overexpression of CC detect CCYPR. Monoclonal or polyclonal antibodies to CCYPR may be CC detect CCYPR. CCYPR itself may be used to detect compounds e.g., CC antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that CC modulate the activity of CCYPR. CCYPR nucleotides can be used in gene cc transgenic animal models of human disease, and can be used in gene CC therapy in target cells with genetic abnormalities with respect to the expression of CCYPR, Diseases which can be diagnosed, treated and CC associated with CCYPR. Diseases which can be diagnosed, treated and cc onclude immune, developmental and cell agonists or antagonists or include anaemia, epilepsy, arteriosclerosis, asthma, cancer, includes include anaemia, epilepsy, arteriosclerosis, asthma, cancer, include anaemia, epilepsy, arteriosclerosis, asthma, cancer, include anaemia, epilepsy, arteriosclerosis, asthma, cancer, include anaemia, disorders of the menstrual cycle and
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disorders
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allergies, diabete infections caused
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08-SEP-1999;
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Lu DAM,
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Baughn M
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R, Patterson
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C, Shah
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Best Local Similarity
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                                                                                                                                                                           Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                        03-APR-2002; 2002US-00029386
                                                                 03-APR-2002;
                                                                                              16-OCT-2003
                                                                                                                        US2003194704-A1
                                                                                                                                                                                                                  Human genome derived single exon probe #9211.
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                                                                                                                                                                                                                                                                                                      ACH76016 standard;
(PENN/) PENN S
(RANK/) RANK D
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0; Mismatches
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3.9e-43;
nes 230;
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AAC10352 standard; cDNA; 340

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AAC10352;

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AAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA 601

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492 61

Matches 169; Query Match

Conservative

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432 TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTTGATCATTTTT 491

TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTGATCATTTTT

CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTTAAACCCCACTTAC CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTTTAAACCCCCACTTAC

551 60

120

Local Similarity

28.0%;

Score 168.4; Pred. No. 2.6 Mismatches

.6e-39; DB 12;

Indels Length Other;

<u>.</u>

Gaps

Sequence 500

seqdata.uspto.gov/sequence.html?DocID=20030194704

BP; 164 A; 71 C; 107 G; 158 T; 0 U; 0

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CC sequences (optionally with conservative amino acid substitutions), an CC isolated antibody that binds specifically to a peptide cited above, CC methods of selling and/or licensing single exon probes or microarrays to CC a customer desiring to measure gene expression, a method of providing CC human gene expression data by subscription, and a computer-readable CC storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe CC cited above. The probe, methods and apparatus are useful in gene CC expression analysis. The probes may be used as tools for surveying CC tisques to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. CC In addition, the probes are used in identifying and characterising CC alternative splicing events, in detecting and characterising gross calternative splicing events, in detecting and characterising gross calternative splicing events, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human CC single exon probe of the invention. Note: The sequence data for this contain the CC format directly from USPO at the contain of the present sequence data for this contain the CC format directly from USPO at the contain the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid probe for measuring human gene CC expression, comprising any of the 27,400 fully defined nucleotide CC expression, comprising any of the 27,400 fully defined nucleotide CC encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that CC hybridises under high stringency conditions to a nucleic acid molecule CC expressed in human cells or tissues. Also included are a spatially-CC addressable set of single exon nucleic acid probes for measuring human CC gene expression (comprising a plurality of single exon nucleic acid CC probes cited above, where each of the plurality of probes is separately CC and addressably isolatable or amplifiable from the plurality), a single CC exon microarray for measuring human gene expression, a wector comprising the single exon CC probe cited above, an ORF-encoded peptide comprising the single exon CC contiguous amino acids of any of the above-mentioned amino acid and contributions of the above-mentioned amino acid of the above-mentioned amino acid and contributions are a spite interior.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; SEQ ID NO 9211; 80pp; English
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diameter forces in contracts.
Drosophila melanogaster expressed polynucleotide SEQ ID NO 16031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 340 BP;
                                           26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wew nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for distance to feature to the sequence tag (5' EST) for well nucleic sequence to 5'ESTs and for more than the sequence to 5'ESTs and the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-500381/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nostic, forensic, gene therapy and chromosome mapping are used to obtain upstream regulatory sequences and
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                                                                                                                                                                                                                                                                                                                                                                                                                           ATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGG
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ilarity 98.8%;
Conservative
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                                           (first
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                                         entry)
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Pred. No. 1.2e-36;
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Matches 262; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 829 BP; 229 A; 208 C; 210 G; 182 T; 0 U;
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11-JUL-2000; 2000US-00614150.
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TCAATAGCCGAATCGCAAGTGGCGCTGAAGTCGATTGTGCAGCCGCATCTCACAGAAAAG
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                                             CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
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                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide comprising any one of CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was CC determined by the technique of SBH (sequencing by hybridisation). Also CC included is a purified polypeptide comprising a sequence corresponding to CC a reading frame of the novel polynucleotide. The nucleic acid sequences CC are useful in diagnostics as expressed sequence tags (EST) for CC identifying expressed genes or for physical mapping of the human genome, CC responsible for genetic disorders and other traits. The nucleotide Sequences are also useful as hybridisation probes, as oligomers for PCR, CC for chromosome and gene mapping, in the recombinant production of CC protein, or in generating antisoned DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data CC obtained in electronic format directly from USBTO at
                                                                                                                  Matches
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                                                                                                                                                                                                                            Sequence 422 BP;
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) DICKSON M C.
) JONES L W.
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CTCCAGGACCCATGGAGTCCTTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAGAAGAAGC
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                                        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the fill 5' UTR is rarely included. 'ESTs are derived from mRNAs with intact 5' ends and can therefore be us to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                      diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein 5'
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                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 14434; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1999;
                               expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACTGAGTAAGATGGCGGGTCGCTCTGTGGCTCATCTTTCATAGATGAGACAAGCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATA
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RESULT 37

AAK56622

ID Human

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Best Local Similarity 98.6
   14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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9-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCACCACCTTAATAGACGAC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTTAATTCCA
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2000US-0198123P

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Pred. No. 5.4e-27;
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08-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                  expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic seguences from the present invention. AAK942 to AAK54990 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                             AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                         Sequence 441 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
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 138
                               99
                                                             78
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM83841.
                             AAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGG
                                                                               CCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1682; 3071pp + Sequence Listing; English.
AGATGGCGGGTCGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAG
                                                                                                                                                                                                                      sequences
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2000US-0249214P
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2000US-0251988P.
; 2000US-0256719P.
; 2000US-0251479P.
; 2000US-0251866P.
; 2000US-0251868P.
                                                                                                                           Conservative
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                                                                                                                                                                                       A; 119 C; 127 G; 89 T; 0 U; 7 Other;
                                                                                                                                                                                                                        used in the exemplification of the
                                                                                                                                       19.7%;
                                                                                                                          3; Mismatches 130;
                                                                                                                                         Score 118.4; DB 4
Pred. No. 1.7e-24;
                                                             CTGCAAGCAGAGAAGAAGCTACTGAGTA
                                                                                                                                                        DB 4;
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9 TCCCGGCGCCGACTCCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAAACCTGG 68

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RESULT 38
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Matches 191;
                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL07182 standard; cDNA; 4406
                                                           Sequence 4406 BP; 1178 A; 1021 C; 1027 G; 1180 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 16028; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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                Score 116; DB 4;
Pred. No. 2.8e-23;
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAQ00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
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Ishii
nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combin of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602
                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                             Claim
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T,
3, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELIX RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAAGCTCCTGAGTAAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGATGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTGTCCCCCGCAGGCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAGGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone (5'-primer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 99JP-00248036.
; 99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                        NO 1556; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           714
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Pred. No. 5.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO:1556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
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combination

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Matches 152;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods AH803166 to AH13628 and AH813633 to AH189742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
     Ota T,
Ishii S,
                                                                                                                            29-UUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-UUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence SEQ ID NO:18986.
                                                                                                                                                                                                                                                                                                                                                                                          EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH18715 standard; cDNA; 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 714 BP; 113 A; 246 C; 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
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                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000EP-00116126
                                                                               (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer;
                             Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTGGACGAGGGCAGCCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTGGATGAAGAGAACATATGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGCCCCGAGCCTACCGCTCCCACCTGCGCAGGATCTGCGAGGGCCTGGGCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGCGTGCTGGCCGCCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis;
     H
                             Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
     Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 111; Indels
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
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No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 4;
l.3e-14;
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  Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 714;
                          Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 578
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                    Claim 8;
                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                    The present invention describes primer
                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                    NO 18986; 2537pp + Sequence Listing;
                                                                                                                                                                                     sets
                                                                                                                                                                                                     English
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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence's eat least 15 nucleotides and the combination of the 5'-end sequence's eat least 16 nucleotides and the combination of gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18742 represent human aclid sequences; AAB2946 to AAB95893 represent human anino acid sequences; and AAH13627 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end present invention for synthesising 5602 full-

Matches Query Match Best Local Similarity Sequence 181 459 121 61 1602 BP; 334 A; 458 CGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGCGTGCTGGCCGCCGGGC CCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGT 398 ACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGACTGCGACTTCCTGGCTGCGCTCT ATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCTTGT TGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCC TAPATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCAC TGTTGGATGAAGAGAACATATGA 601 ACGGCCCCGCCGAGCCCTACCGCTCCCACCTGCGCAGGATCTGCGAGGGCCTGGGCCGGA ATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAA Conservative 14.2%; 0; Score 85.4; DB 4; Pred. No. 2e-14; C; 491 G; 319 T; 0 U; 0 Other; Mismatches 111; Indels Length 1602; 0 Gaps 578 518 240 180 458 60 120

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XXXXXXXXXXXXXX
                                 Human;
                     splice variant; transcriptome; oligonucleotide library;
                                                                                                                                ABN50404 standard; DNA; 60
                                                                                 15-JUL-2002
                                 mouse; rat; splice transcript; detection; RNA transcript;
                                                                                 (first entry)
                                                        transcript
                                                         detection oligonucleotide
                                                         SEQ ID NO:23152
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RESULT 43
ACF25360
ID ACF25
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABM27253 to ABM59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular libraries to detect transcripts of a sub-transcriptome under a particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                 Rattus norvegicus
                                                 spinal cord; neuropathic pain;
analgesic; gene therapy; gene;
                                                                                                      Rat microtubule associated protein IB gene
                                                                                                                                                                                                                   ACF25360 standard; DNA; 7095 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000; 2000US-0221607P
02-MAY-2001; 2001US-0287724P
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                                                                                                                                            22-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      messenger RNAs transcribed from a given transcription unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 23152; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-257383/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-2001; 2001WO-IB001903
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                                                                                                                                                                                                                                                                                                                            199 GAAGGAGGCAGAGAAGATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                           GAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 22 A; 14 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wasserman
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yecification, but was obtained in electronic format
ftp.wipo.int/pub/published_pct_sequences
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Pred. No.
                                                                      central sensitisation pain; pain;
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hes 0;
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Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                downregulated in the spinal cord of a mammal in response to mechanically distinct first and second models of neuropathic or central sensitisation pain, useful in the screening of compounds for diagnosing or treating pain. A protein encoded by a gene of the invention has analgesic activity. A polynucleotide of the invention may have a use in gene therapy. The gene sequence is useful for preparing a composition for diagnosing or treating pain. The present sequence represents a gene of
                                        alternative splicing event; genomic alteration
                                                                                                                    29-JUL-2004
                                                                                                                                                  ACH78513;
                                                                                                                                                                               ACH78513 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7095 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated gene sequence that is downregulated in the spinal cord of a mammal in response to mec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 125-127; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of an isolated gene sequence diagnosing or treating pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brooksbank
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07-FEB-2002; 2002GB-00002883
                                                          Human; probe; ss;
                                                                                      Human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 TCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGA
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                                                                                                                                                                                                                                                        GAACCCAAAAAGGAGATTAAGAAGA 1909
                                                                                                                                                                                                                                                                                    GCATTGATGGAGAAATTTAAGAAGA
                                                                                                                                                                                                                                                                                                                   AAGGACGCCAAGAAGGAGGTGAAGAAAGACGAGAAGAAGAAGTTAAAAAAGGAAGAGAAG 1884
                                                                                                                                                                                                                                                                                                                                                 AAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                           GTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACCCGAAGAAAAGAAAGAGGAGAAGCCCAAGAAGGAAGTGGCTAAAAAAGGAAGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                    derived single exon probe #11708
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dixon AK,
                                                        gene expression; single exon probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2124 A; 1856 C; 1799 G; 1316 T; 0 U; 0 Other;
                                                                                                                                                                               DNA; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%;
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16-OCT-2003 US2003194704-A1

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                                                                                                                                                                                                                                                                     comeasuring human gene expression, a vector comprising the single exon contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an ci isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing thuman gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe controlled above. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising calternative splicing events, in detecting and characterising gross alternations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained conclusionated in electronic format directly from USPTO at sequence.
                                                                                                                                                                            Query Match
Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                              Sequence 543 BP; 137 A; 128 C; 119 G; 159 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; SEQ ID NO 11708; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridises under high stringency conditions to a nucleic acid molecexpressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human cells or tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-119264/12
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(RANK/) RANK D
    61
                                                                                                                                                                                              Similarity
                                         ATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACAAAA 578
                                                                                                                         ATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCTTGT
ATAGTCTGGATGGAGACTGTAGGCCCAACCTCAAGAGGATTTGTGAAGGAATCAATAAGT
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Pred. No.
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Query Match

Local Similarity

Conservative

55.4%; 7.1%;

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0.36;

66;

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Gaps

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DB 6;

Length 15790; Indels

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                                                                   CC Candida spp. sequences that are differentially expressed in a pathway continuing and continuing and continuing and continuing are differentially expressed in a pathway continuing the pathway or continuing the pathway of the continuing and compositions, continuing a medicament for treating, preventing and/or alleviating continuing a medicament for treating, preventing and/or alleviating continuing a medicament for treating, preventing and/or alleviating continuing a medicament for treating and or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds cor polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, this sequence represents a polynucleotide associated with the Bax gene continuing against the bax gene continuing against presents and continuing against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
neurodegeneration; cell death; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 36; Fig 2; 344pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-667002/71.
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04-JAN-2001; 2001EP-00870002.
09-JAN-2001; 2001EP-00870003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bax gene. The Bax gene of the invention is useful for identifying Bresistant yeast or fungi, identifying, or obtaining and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel nucleic acid representing a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABG93349.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JANC ) JANSSEN PHARM NV.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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US-09-949-016-23836

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Sequence 12813, Ap
Sequence 12906, A
Sequence 2813, Ap
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| US-09-949-016-17640-8128
| US-09-949-016-17649
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NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 537
LENGTH: 1175
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Best Local Similarity
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APPLICANT: Tang, Y. Tom
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CURRENT APPLICATION NUMBER: US/09/799,451
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TITLE OF INVENTION: No. 6783969e1
TITLE OF INVENTION: Polypeptides
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ORGANISM: Homo sapiens
FEATURE:
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390 CCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTG 449
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Goodrich, Ky.
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
                                GTGCCATGACGGCACTTAGCTTTGGTGAGGTAGACTTCACCTTCGAGGCTGCTGTTCTGG
                                                               TTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTAT 389
                                                                                                  GCTCCTTTGGCCCCAGTGAGCTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGG
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Yang, Yonghong
Wehrman, Tom
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Chen, Rui-hong
Wang, Zhiwei
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Ghosh, Reena
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SEQ ID NO 14427
LENGTH: 340
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                                                                                                                                                                                       Matches
                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: k=g FEATURE:
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
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LOCATION: 208
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: r=a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 166
OTHER INFORMATION: r=a
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                                                                                                                                                                                                                                                                                       LOCATION:
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TCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGA
                                                                        TGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGC 164
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                                                                                                                       ATGTCTTTAATTCCAAAAACCTGGCCGKTCAGGCACAAAARAAGATCTTGGGTAAAATGG
                                                                                                                                          ATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGG
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                                                     TGTCCAAATCCATCGCCACCATCTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGC
                                                                                                                                                                                      Conservative
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Pred. No. 4.7e-40;
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US-09-513-999C-14434
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Best Local (
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SEQ ID NO 14434
LENGTH: 252
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TITLE OF INVENTION: Expressed Sequence Tags
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14434, Appearent No. 6783961
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ORGANISM: Homo sapiens
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                               APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECON
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CLASSIFICATION: 435
                                 APPLICATION NUMBER:
                                                                                                                                                              COUNTRY:
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o. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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Alexandria
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98.6%;
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                                                                                                                                                                                                                  Suite 500
                                                                Version
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RESULT 5
US-09-248-796A-4857
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                              Sequence 4857, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:
TITLE OF INVENTION: NOTAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
SEQ ID NO 4857
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Best Local 9
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INFORMATION FOR SEQ ID NO:
                  NUMBER OF SEQ ID NOS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHAX: (703)683-4109
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1271
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RESULT 7
US-09-436-699C-19
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US-09-489-039A-1361
; Sequence 1361, Application US/09489039A
; Patent No. 6610836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1361
LENGTH: 804
TYPE: DNA
ORGANISM: Klebsiella
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PNEUMONIAS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
ERIOR APPLICATION NUMBER: US 60/117,747
UNMBER OF SEQ ID NOS: 14342
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NAME/KEY: unsure
LOCATION: (50)
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                                                                                                                               AGGAAAAACTGGAAAAAGATCCGCGCATCGCTGCCACCATGGCGAACGCCCAGAAAGGCG
                                                                                                                                                             AGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGG 362
                                                                                                                                                                                                                                TCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGG 302
                                                                                                                                                                                                                                                                 CCGCCAGCCCGAACAAAGAGCTGGCCAAAGAGTTCCTCGAAAACTACCTGATGACCGATC
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Pred. No. 0.014;
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Complete Genome Patent No. 6503729
TITLE OF INVENTION: jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Office 97
SEQ ID NO 19
LENGTH: 1719
TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (84808)...(84808)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
LOCATION: (84812)...(84812)
OTHER INFORMATION: n equals a
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
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APPLICANT: Simmons, Carl
ITILE OF INVENTION: Plant Aminoacyl-trna Synthetases
FILE REFERENCE: BBL266 US NA
CURRENT APPLICATION NUMBER: US/09/436,699C
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 60/107,276
PRIOR APPLICATION STATE: 1998-11-05
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1996
NUMBER OF SEQ ID NOS: 3
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                                                                                                               NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (28222)...(28222)
OTHER_INFORMATION: n equals
                                                                                                                                                                         OTHER INFORMATION: n equals
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LOCATION: (28257)..(28258)
                                                                                                                                                                                                                                                                                                              ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
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LOCATION: (309398). (309398)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (309418). (309418)
OTHER INFORMATION: n equals a, t
                                                                 LOCATION: (559241)...(559241)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (600992)...(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (319226) ... (319226)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (191995) .(191995)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (98159)..(98159)
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OTHER INFORMATION: n equals
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LOCATION: (312837)...(312837)
OTHER INFORMATION: n equals
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LOCATION: (231980)..(231980)
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OTHER INFORMATION: n equals a,
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LOCATION: (983
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; OTHER INFORMATION:
US-08-916-421B-1
          DTHEK INFO..... feature
NAME/KEY: misc_feature
LOCATION: (1664854)...(1664855)
LOCATION: n equals a,
                                            NAME/KEY: misc_feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals a,
                                                                             LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
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LOCATION: (1310988)..(1310988)
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US-09-692-570-1/c
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TITLE OF INVENTION: Complete Genome Sequence
Patent No. 6797466
TITLE OF INVENTION: jannaschii
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals
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LOCATION: (98239)..(98239)
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LOCATION: (98159)..(98159)
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LOCATION: (98120)..(98120)
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LOCATION: (84808)..(84808)
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LOCATION: (191995)..(191995)
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LOCATION: (559241)...(559241)

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LOCATION: (319226)...(319226)
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LOCATION: (234720)..(234220)
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NAME/KEY: misc_feature
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(1096846)..(1096846)
                                         NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
                                                                                     NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (1115881)..(1119881)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
(1084830)..(1084830)
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LOCATION: (871619)..(871619)
OTHER_INFORMATION: n equals
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
         NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals
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LOCATION: (779455)..(779455)
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LOCATION: (741684)..(741684)
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals
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LOCATION: (674435)...(674435)
OTHER INFORMATION: n equals
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LOCATION: (657081)..(657081)
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RESULT 10
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
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; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
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Best Local Similarity
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Best Local Similarity
Matches 104; Conserv
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Giordano, J.Y TITLE OF INVENTION: ESTS
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APPLICANT: Jobert, S.
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LOCATION: 235..399
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ASKKYMWKRWWWCWARMYRYSTGTRASMWWRRWYYTMMKWWKYAWARAAWRWWAMWAW
                               ANACCCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATA
                                                               KAWRASCYMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWY
                                                                                               TTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTT
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; LOCATION: (1)...(161900)
; OTHER INFORMATION: n = A
US-09-949-016-12685
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US-09-949-016-12685/c
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                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                 SOFTWARE: Fast
SEQ ID NO 12906
                                                                                                                                                                                                                                                                                                                                                         Sequence 12906, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12685
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                 PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                            NUMBER OF SEQ ID NOS:
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                                                                                PRIOR FILING DATE:
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                                                                                2000-09-08
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                                         Windows Version
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APPLICANT: BOETS, Annemie
APPLICANT: ANNAUT, Greta
APPLICANT: VAN RIE, Jeroen
APPLICANT: DAMME, Nicole
TITLE OF INVENTION: NO. 6706860el Toxins
FILE REFERENCE: 021565-091
CURRENT APPLICATION NUMBER: US/09/858,525B
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 09/573,872
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 12
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US-09-858-525B-9
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                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 82; Conserv
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LENGTH: 2520
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Best Local Similarity
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LOCATION: (3)..(2510)
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OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: modified DNA encoding ISP1A protein
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                  417 AAGCTGTTCAAGATCGACTCCCAGAACCACTCCCAGCAGCAGCAGCAGGACGAGCTGAGG
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                         218 ATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCAT 255
                                                                                                                                                                     98 AAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGGGGGGGCTG
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                                                                                                    GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATC 217
                                                                                                                                       AAGATCGAGTACCAGTCCGACGACGCCCTGCACATCGACAACAAGATCTTCAAGGAGCTG
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Pred. No. 11;
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RESULT 14 US-09-270-767-7337/c ; Sequence 7337, Application US/09270767 ; Patent No. 6703491

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US-09-270-767-22619/c
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; ORGANISM: Drosophila melanogaster
US-09-270-767-7337
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 22619
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference; 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7337
                                                        Sequence 23836, Application US/09949016 Patent No. 6812339
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Best Local (
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Best Local (
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83; Conserv
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                                                                                                                                                             GÍTGAÍTACTTGTÁAÁTACGTTTTGTCÁGCTTGÁAACCGCA 238
                                                                                                                                                                                              TTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCA 546
                                                                                                                                                                                                                               TTGACCATAGATTTAAATCAATACATTGCGACAATAATACATTGACGTTGGCAACAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 23836
LENCTH: 601
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 173088
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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304 GAAATTTAAGAAGAAAGTTCATCAGCTTGCTAT 336
                                                                           244 CAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGA 303
                                                                                                                                                        184 СТАСАСССАЛАЛСАЛСАЛСБАССАСАСАСАЛАГАТСАЛСАЛССТСАТСАЛСАСАСТСАТ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 TTATGTGGCCAACAACATATGAGGAAAAAGCTCAACATCGCTGATCTTTAGAGAAAATT
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                                                                                                                                                                                                                    Similarity
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                                       TTATGTGGCCAACAAACATATGAGGAAAAAGCTCAACATCGCTGATCTTTAGAGAAAATT
                                                                                                                  GAACAACACCATCAAAAAGTAGGCAAAGGATATAAACAGTCACTTCTCAAAAGAAGACAT
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llarity 52.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                               for Windows Version
                                                                                                                                                                                                              6.0%;
52.3%;
                                                                                                                                                                                             Score 36.2; DI
Pred. No. 0.5;
0; Mismatches
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US-09-596-002-15
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SEQ ID NO 15
LENGTH: 28626
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Patent No. 6673910
GENERAL INFORMATION:
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                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILLING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                     NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                         ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                          TYPE: DNA
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18032 ATAATAAATTTGCCTCTAGTGTATCATGCCCTTGATC 18068
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                                 341 GIGGICAGTITCCATCAGGIGGATTATACCTITGACC 377
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                                                                                                    281 CAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACC 340
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Berg, Kim,
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                                                                                                                                  Score 36.2; DI
Pred. No. 5.1;
0; Mismatches
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US-09-949-016-12028
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-16647
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                                                                                           US-09-949-016-12028
                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 12028
LENGTH: 32043
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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LENGTH: 32039
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                                            Query Match
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  Matches
                         Best Local Similarity
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TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR RPPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                                                                                                                   ORGANISM: Human
                                                                                                                                        TYPE: DNA
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    Conservative
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52.3%;
                     52.3%;
Score 36.2; DB Pred. No. 5.4; 0; Mismatches
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RESULT 23
US-09-949-016-17033/c
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US-09-949-016-17032
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                                                                                                                         GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                               Sequence 17033, Application US/09949016 Patent No. 6812339
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Best Local Similarity
Matches 97; Conserv
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SEQ ID NO 17032
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTATGTGGCCAACAAACATATGAGGAAAAAGCTCAACATCGCTGATCTTTAGAGAAAATT 17487
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Pred. No. 21;
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                     RESULT 25
US-09-167-109-3
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US-09-248-796A-11532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAY
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 17033
LENGTH 194937
TYPE: DNA
  Sequence 3, Application US/09167109
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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LENGTH: 603
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Patent No. 6747137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                             249
                                                                                                                                                                                                                             189 CCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGC
                                                                                                                                                                                                                                                                       309 TGATATACAACAAAATGAGTTÄAGCGAAAGCGATTCAAGTGAAÄATGATTTAAGÄGAAAT
                                                                                                                                                                                                                                                                                                              129 TAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 ATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACC 190
                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                               TGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGA 285
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                                                                                                        TGGTCATGATTCATATGAATGTTCACTGGCATTTAGA 465
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51.6%;
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48.7%;
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Pred. No. 0.9;
0; Mismatches
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Pred. No. 21;
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맑 Ş В S 밁 Ş 밁 8

Length 603;

Indels

<u>,</u>

Gaps

0

248 368

Patent No. 6399297

INFORMATION:

TRAF EXPRESSION

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; LOCATION: (218)..(1924)
; PUBLICATION INFORMATION;
; DATABASE ACCESSION NUMBER: U21092
; DATABASE ENTRY DATE: 1995-03-23
US-09-167-109-3
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APPLICANT: Cowsert, Lex M.
APPLICANT: Monia, Brett P.
APPLICANT: X1, X1aoxing S.
TITLE OF INVENTION: ANTISENSE MODULATION OF TR
FILE REFERENCE: ISPH-0321
CURRENT APPLICATION NUMBER: US/09/167,109
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                              US-09-949-016-468
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 468
LENGTH: 2455
                                                                                        Matches
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                                                                                                            Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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ORGANISM: Homo sapiens
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                                    72 TTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAA 131
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TTGAGAGACAAAAGGAAATGCTTCGAAATAATGAATCCAAAATCCTTCATTTACAGCGAG 1181
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                                                                                                                                                                                                                                                                                                            207012
                                                                                 Score 35.4; DB Pred. No. 2.1; 0; Mismatches
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Pred. No. 2.1;
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US-09-949-016-4366
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US-09-949-016-4366
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                                                                 SOFTWARE: Fast
SEQ ID NO 4366
LENGTH: 7571
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMEER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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LENGTH: 2455
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Matches 81; Conserv
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APPLICANT: Baltimore, David
APPLICANT: Cheng, Genhong
APPLICANT: Ye, Zheng-Sheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4366, Application US/09949016 Patent No. 6812339
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APPLICANT: Cleary, Alleen
TITLE OF INVENTION: Truncated Craf-1 Inhibits CD40 Signalling
FILE REFERENCE: 0575/50659
FILE REFERENCE: 0575/50659
CURRENT APPLICATION NUMBER: US/08/813,323C
CURRENT FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                               NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                    ORGANISM: Human
                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1122 TTGAGAGACAAAAGGAAATGCTTCGAAATAATGAATCCAAAAATCCTTCATTTACAGCGAG 1181
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                                                                                                                     FastSEQ for Windows Version
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US-09-566-921-32
; Sequence 32, Application US/09566921
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; LOCATION: 8083
; OTHER INFORMATION: a;
US-09-976-594-725
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LENGTH: 8146
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTMARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Furness, APPLICANT: Buchbin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Incyte ID No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                   TATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAG 316
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Pred. No. 4.
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 Query Match
                                                                                                                                                                                         SEQ ID NO 16108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16108, Ap
Patent No. 6812339
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                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Bdwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001307
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6682888 475473.1
NAME/KEY: unsure
LOCATION: 9384, 10290-10321, 10325
                                                   FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: (1)...(101300) OTHER INFORMATION: n = A
                                                                                                                                   ORGANISM: Human
                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                       LENGTH: 101300
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Local Similarity 46.8%;
les 111; Conservative
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Pred. No. 5.4;
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US-09-949-016-17590
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Secretic Reference: 38-10(15849)B
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION UNMER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                  US-09-902-540-8128
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FRStSEQ for Windows Version
SEQ ID NO 17590
LENGTH: 247299
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                       Sequence 8128, App
Patent No. 6833447
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           89590 GAAGAGAAGAAGTGAAAAAGGAAAAGGAAAAGGAACCCAAAAAAAGAAATTAAGAAG 89646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 GAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GCTCTACAGAGTGACCAGGGAGTACACCCCAAAACAAGAAGGAGGCAGAGAAGATCATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111; Conservative
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ilarity 56.4%;
Conservative
                                                                                                                                                                                                                                                                Application US/09902540
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0; Mismatches
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US-09-902-540-832/c
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15849)
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 832
LENGTH: 8352
TYPED: NAM
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SEQ ID NO 8128
LENGTH: 2455
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
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4430 ATTG 4427
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                                    329 CTTG 332
                                                                                                        269 AATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAG 328
                                                                                                                                                                                 209 GAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAAT 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCACGCGCGTCAAGAAGCAGATGGAGAAGACCCAGAAGGAGTACTACCTGAATGAGCAG
                                                                       ATGCAGGCCATTCAGAAGGAGCTGGGTGAGCGCGACGAGTTCAAGAACGAGATTCAGGAG
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Pred. No. 5;
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RESULT 35 US-09-949-016-13146

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US-09-949-016-194263
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                                                                                                                                                             ; ORGANISM: Human US-09-949-016-194263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 194263
LENGTH: 601
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SEQ ID NO 13146
LENGTH: 58829
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GENERAL INFORMATION:
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Patent No. 6812339
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J.
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LOCATION: (1)...(58829)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                       TYPE: DNA
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  TGTCTATATTTATATCTAACATCAGGGCTCCCAGATATATAAAGCAAATATGGAGAGAAG
                                  TGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGG 152
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                                                                                                 5.8%;
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Pred. No. 1.2;
0; Mismatches 10
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Pred. No. 16;
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US-09-949-016-14033/c
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; ORGANISM: Human
US-09-949-016-17262
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
Sequence 14033, Application US/09949016
Patent No. 6812339
GENERRAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIC
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: VENTER, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 20701;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 TGCTGGATGAGCTCTACAGAGTGACCAGGGGAGTACACCCCAAAACAAGAAGGAGGCAGAGA 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTATAGGAATAATC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAGCAAGATGTACACAGCAATACAATAATTATCAACTCTAAGACCCCCATTTGCAATAC
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Pred. No. 11;
0; Mismatches 100;
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                                                                                                                  DETECTION
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PRIOR APPLICATION NUMBER: 60/237,768

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RESULT 40
US-09-949-016-205411/c
US-09-949-016-205411, Application US/09949016
; Sequence 205411, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
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; Sequence 205410, Application US/09949016
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local S
Matches 56
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Best Local S
Matches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 205410
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
-09-949-016-205410
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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NAME/KEY: misc_feature
LOCATION: (1)...(784019)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                            ANGGACACCATCANGANAGTGANANAGACGGCCCACAAGTTGGANGANAATACTTGCANAT
                                                                                                                                                                         CATGYATAGCACTTTTGATGGTAAACTTGAGGAAGACATTT 264
                                                                                                                                                                                                          CAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTT 322
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Pred. No. 8
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   KNOWN GENES
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   ASSOCIATED
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OF DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VIMMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 205411
LENGTH: 601
TYPE: DNA
RESULT 42
US-09-908-988B-5
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SOFTWARE: FRATSEQ for Windows
SEQ ID NO 17549
LENGTH: 24345
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Best Local
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Local Similarity 58.8%;
                                                                                                                                                                       13643
                                                                                                                           281 CAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTT 322
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                                                                                                                                                                       AAGGACACCATCAAGAAAGTGAAAAGACGGCCCACAAGTTGGAAGAAAATACTTGCAAAT 13702
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Pred. No. 1.4;
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Pred. No. 13
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Sequence 5, Application US/09908988B Patent No. 6740751

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RESULT 43
US-09-248-796A-80
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                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR ETLING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: OLSON, ERIC
APPLICANT: SPENCER, JEFFREY A.
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
CURRENT FILING DATE: 2000-07-18
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                   Query Match
Best Local Similarity
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SEQ ID NO 5
LENGTH: 1597
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                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mus musculus
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LOCATION: (299)..(1327)
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Local Similarity 53.3%;
les 73; Conservative
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566 GGTATCAACAAAATGTTGGATGAAGAGA 593
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                                       AAAAACGCCGAAAAGTATCACTTGGAGGAATATAAACAAAATTTTATCGAACAATTGAAT
                                                                                                                    ATTGATAAGGCATATGTATTAGTTGAACATAAATTTCAAGAATTATGGGAAAATGCATCG
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                                                                            TIGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGAT 565
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Pred. No. 2.9;
0; Mismatches
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Pred. No. 2;
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LENGTH: 2349
TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Best Local
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT APPLICATION NUMBER: US/0
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/241,755
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ORGANISM: Homo sapiens
                                                                                                                                                                   ORGANISM: Human
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                                   158 GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATC 217
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GAGGAGCTACGCCAGGCGCTGGAGAAGTTCGAGGAGTCCAAGGAGGTGGCAGAAACCAGC 615
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ilarity 59.0%;
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                                                                      Score 34.4; DF Pred. No. 4.2; 0; Mismatches
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Search completed: July 28, 2005, 19:03:54 Job time : 187 secs	616 ATGCACAACCTCCTGGAGACTGACATCGAGCAGGTGAGTC 655	218 ATCAAGAACCTCATCAAGACAGTCATGAGCTGGCCATTC 257

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1: /cgn2=6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2-6/ptodata/2/pubpna/US07 NEW PUB.seq:*

3: /cgn2-6/ptodata/2/pubpna/US07 NEW PUB.seq:*

4: /cgn2-6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2-6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2-6/ptodata/2/pubpna/US08 NEW PUB.seq:*

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9: /cgn2-6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

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12: /cgn2-6/ptodata/2/pubpna/US109 NEW PUB.seq:*

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15: /cgn2-6/ptodata/2/pubpna/US10B PUBCOMB.seq:*

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US-10-372-876-98

US-10-755-889-215

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17 US-10-242-515-2333
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20 US-10-682-915-9
                                                                                              19 US-10-755-889-39
10 US-10-087-192-866
16 US-10-087-192-493
13 US-10-087-192-493
13 US-10-087-192-493
14 US-10-087-192-493
15 US-10-087-192-493
16 US-10-087-192-3207
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19 US-10-263-929-36
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Sequence 39, Appl
Sequence 493, App
Sequence 493, App
Sequence 2914, Ap
Sequence 3207, Ap
Sequence 3207, Ap
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Sequence 3207, Ap
Sequence 2801, Ap
Sequence 2801, Ap
Sequence 2801, Ap
Sequence 2801, Ap
Sequence 5724, Ap
Sequence 572
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Sequence 1, Application US/10627571

Publication No. US20040082771A1

GENERAL INFORMATION:
APPLICANT: KASID, Usha N.
APPLICANT: KUMAR, Deepak
APPLICANT: KUMAR, Deepak
APPLICANT: GOKHALE, Prafulla
APPLICANT: HAMAD, Imran
ITITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
ITITLE OF INVENTION: THEREOF
FILE REFERENCE: 22316
CURRENT APPLICATION NUMBER: US/10/627,571
CURRENT APPLICATION NUMBER: US 60/264,062
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR APPLICATION NUMBER: DET/US02/02212
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
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; NAME/KEY: misc feature
; OTHER INFORMATION: SCC-S2
US-10-627-571-1
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Best Local Similarity 100.
Matches 601; Conservative
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                         GGAGTACACCCAAAACAAGAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGT
                                                                                                      CACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAG
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GGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGT
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3 US-10-087-192-1105
10 US-10-425-115-13759
10 US-10-335-977-319
8 US-10-335-977-3200
10 US-10-672-787-15
10 US-09-880-107-2380
11 US-10-741-600-17795
12 US-10-424-599-109224
12 US-09-864-761-18684
12 US-09-864-761-1935
12 US-10-719-993-7050
13 US-10-719-993-6864
14 US-10-719-993-6864
15 US-10-741-601-5611
16 US-10-087-192-2002
17 US-10-087-192-23404
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                                                                                                                                                                                                                                                                                                                                                                                       Length 1915;
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APPLICANT: Lia, Congfen
APPLICANT: Liao, X. Charlene
APPLICANT: Liao, X. Charlene
APPLICANT: Liao, X. Charlene
APPLICANT: Masuda, Esteban
APPLICANT: Pardo, Jorge
APPLICANT: Pardo, Jorge
APPLICANT: Zhao, Haoran
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Modulators of Lymphocyte Activation and Migration
FILE REFERENCE: 021044-000330US
CURRENT APPLICATION NUMBER: US/10/491,545A
CURRENT FILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: human TNF-induced ; OTHER INFORMATION: complete CDS US-10-491-545A-48
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SEQ ID NO 48
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48, Application US/10491545A Publication No. US20050130117A1
                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                          Matches 600;
                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                          97.9%;
                                                                                                                                                                                          0;
                                                                                                                                                                                        Score 588.4; DB 22;
Pred. No. 2.3e-165;
0; Mismatches 1;
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                                                                                                                                                                                                                              Length 1892;
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CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: PCT/US98/27059
PRIOR PELLING DATE: 1996-12-17
PRIOR PELLING DATE: 1998-12-17
PRIOR PELLING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,007
PRIOR APPLICATION NUMBER: 60/068,007
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,057
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLING DATE: 1997-12-19
PRIOR PELLING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,369
PRIOR PELLING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR PELLING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,068
PRIOR APPLICATION NUMBER: 60/068,069
PRIOR APPLICATION NUMBER: 60/068,069
PRIOR APPLICATION NUMBER: 60/068,063
PRIOR APPLICATION NUMBER: 60/068,063
PRIOR APPLICATION NUMBER: 60/068,063
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PILING DATE: 1997-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application US/10097065
Publication No. US20030055236A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Moore, Paul A. et al.
TITLE OF INVENTION: 110 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE: PZ021P1
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                    NUMBER: 60/068,008
                                         1997-12-18
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; LOCATION: (1934)
; OTHER INFORMATION:
US-10-097-065-98
Sequence 98, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/068,365
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 98
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Best Local Similarity
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LOCATION: (1926)
OTHER INFORMATION: r
NAME/KEY: SITE
LOCATION: (1928)
OTHER INFORMATION: r
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TYPE: DNA
ORGANISM: HOMO E
FEATURE:
NAME/KEY: SITE
LOCATION: (161)
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                    Application US/10372876
No. US20030204071A1
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Pred. No. 2.7e-165;
0; Mismatches 4;
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FILE EFFERENCE: P2021P1

CURRENT APPLICATION NUMBER: US/10/372,876

CURRENT FILING DATE: 2003-02-26

PRIOR APPLICATION NUMBER: 09/334,595

PRIOR FILING DATE: 1999-06-17

PRIOR PLING DATE: 1998-12-17

PRIOR PLING DATE: 1998-12-17

PRIOR FILING DATE: 1997-12-18

PRIOR PLING DATE: 1997-12-18

PRIOR PLING DATE: 1997-12-18

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR PLING DATE: 1997-12-18

PRIOR PLING DATE: 1997-12-18

PRIOR PLING DATE: 1997-12-18

PRIOR PLING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,369

PRIOR PLING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,369

PRIOR PLING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,369

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Best Local Similarity
Matches 590; Conserv
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NAME/KEY: SITE
LOCATION: (1934)
OTHER INFORMATION: n e
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LOCATION: (1928)
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                CTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAA
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                                                                                           ACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAG
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CTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAA
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Pred. No. 2.7e-165;
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; SEQ ID NO 215
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-215
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US-10-755-889-215
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Best Local Similarity
Matches 565; Conserv
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nilarity 99.8%;
Conservative
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Sequence 215, Application US/10755889

Publication No. US20040171823A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDES AND POLY
ITILE OF INVENTION: PATHWAY
ITILE OF INVENTION: PATHWAY
ITILE OF INVENTION: MATHWAY
ITILE OF INVENTION: PATHWAY
ITILE OF INVENTION: PATHWAY
ITILE OF INVENTION: POLYNUCLEOTIDES AND POLY
ITILE OF INVENTION: POLYNUCLEOTIDES AND POLY
ITILE OF INVENTION NUMBER: US/10/755,889
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
                                                                                                             TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAAGTTCATCAGCTTGCTA
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TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTTATCCAGGC 395
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Pred. No. 3.6e-158;
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RESULT 6
US-10-755-889-217
US-10-755-889-217
; Sequence 217, Applicat
; Publication No. US2004
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-05-12
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin version 3.2
SEQ ID NO 217
LENGTH: 2003
CORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: MORIS, DAVID W.

APPLICANT: Engelhard, Eric K.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND ME.

TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR PILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059
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US-10-087-192-497
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Best Local Similarity 99.8%;
Matches 565; Conservative
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TYPE: DNA
ORGANISM: Homo sapiens
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516 TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA 575
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Pred. No. 3.9e-158;
0; Mismatches 1;
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLY
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: D0284 NP
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTIN PATENTAL PRIOR BATENTAL P
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US-10-755-889-39
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Best Local Simi
Matches 565;
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ORGANISM: Homo sapiens
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No. US20040171823A1
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Pred. No. 4e-158;
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
VIMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 496
LENGTH: 58723
TYPE: DNA
ORGANISM: Homo sapiens
US-10-087-192-496
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US-10-087-192-496
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Publication No. US20020182586AI
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Bric K.
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Best Local Similarity 99.8%;
Matches 565; Conservative
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
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                                                                                                                   AAATGTTGGATGAAGAGAACATATGA
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Pred. No. 3e-157;
0; Mismatches 1;
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Best Local
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 22914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22914, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
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FEATURE:

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4

OTHER INFORMATION: EXT HUMAN HIT: AL549492.1, EVALUE 0.00e+00

OTHER INFORMATION: NT HIT: 931390, EVALUE 2.60e-01

OTHER INFORMATION: NT HIT: 937657123, EVALUE 0.00e+00
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TYPE: DNA
ORGANISM: Homo sapiens
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                                  AAAT 579
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Pred. No. 7.1e-152;
); Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
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US-10-087-192-493
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Best Local S
Matches 494
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
TITLE OF INVENTION: CANCER
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                   TATCAACAAAATGTTGGATGAAGAAGAACATATGA
                                                                                            GGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGG
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o. US20020182586A1
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Pred. No. 1.1e-121;
0; Mismatches 80;
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 494
LENGTH: 2087
TYPE: DNA
ORGANISM: Mus musculus
US-10-087-192-494
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Best Local Similarity
Matches 490; Conserv
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA
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                                                                                                                                         CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
 AAATGTTGGATGAAGAGAACATATGA 1073
                    AAATGTTGGATGAAGAGAACATATGA
                                                                             TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                              CTCACGGACGGGTTAATAATGTCTTTGACCATTT
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                                                            TGTACAATCCCTTTGGAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGCATCAACA
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Pred. No. 4.2e-122;
0; Mismatches 76;
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RESULT 13 US-09-796-692-3207

US-10-040-862-3207

Sequence 3207, Application US/10040862

Publication No. US20030078396A1

; GENERAL INFORMATION:

RESULT 14

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PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR PPLICATION NUMBER: 60/200,545
PRIOR PPLICATION NUMBER: 60/200,545
PRIOR PPLICATION NUMBER: 60/200,303
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR PPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/221,903
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-04
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PRIOR PRIOR PRIOR DATE: 2000-08-04
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3207
LENGTH: 287
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/223,378 PRIOR FILING DATE: 2000-08-07
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                            492 CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTT
                                                                                                                       432 TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTT
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                                                                                        TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTTGATCATTTTT
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99.7%;
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Pred. No. 6.7e-75;
0; Mismatches 1;
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US-10-057-475B-3207; Sequence 3207, Application US/10057475B; Publication No. US20040002068A1
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; ORGANISM: Homo
US-10-040-862-3207
                                                          RESULT 15
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Best Local Similarity
Matches 286; Conserv
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SEQ ID NO 3207
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TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
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FILING DATE: 2000-05-04
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FILING DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
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FILING DATE: 2000-04-28
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Algate, Paul A.
                                                                                                                                  CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTT 538
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Pred. No. 6.7e-75;
0; Mismatches 1
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RESULT 16
US-10-154-884B-3207
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; Publication No. US20040005561A1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-3207
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NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
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Best Local Similarity
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
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APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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FILING DATE: 2000-04-28
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                       492 CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTT
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                                                                                                          432 TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTT
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Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
                                                                                  TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTTGATCATTTTT
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Algate, Paul A.
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Clapper, Jonathan
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 285.4; DB 17;
Pred. No. 6.7e-75;
0; Mismatches 1;
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RESULT 17
US-10-764-324-3207
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; ORGANISM: Homo sapiens
US-10-154-884B-3207
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PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
Sequence 3207, Application US/10764324
Publication No. US20040175739A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
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Best Local Similarity
Matches 286; Conserv
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-015521US
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CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
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OR APPLICATION NUMBER: US 60/200,303

IOR FILING DATE: 2000-04-28

IOR APPLICATION NUMBER: US 60/200,779

IOR FILING DATE: 2000-04-28

IOR APPLICATION NUMBER: US 60/200,999

IOR FILING DATE: 2000-05-01
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Retter, Marc W.
Corixa Corporation
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Pred. No. 6.7e-75;
0; Mismatches 1;
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Sequence 2801, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mandion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077, 001200
CURRENT APPLICATION NUMBER: US/09/796,692

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TITLE OF INVENTION: Compositions and Methods for the Det TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013520US

CURRENT APPLICATION NUMBER: US/10/764,324

CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: US/10/040,862

PRIOR FILING DATE: 2001-11-06

PRIOR PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-03-07

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR PILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28
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RESULT 18
US-09-796-692-2801/c
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
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Best Local S
Matches 286
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SEQ ID NO 3207
LENGTH: 287
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ORGANISM: Homo sapiens
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CURRENT FILING

DATE:

2001-03-01

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Sequence 2801, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Metter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Hematological Malig
FITLE REFERENCE: 014058-013520US
FILE REFERENCE: 014058-013520US
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US-10-040-862-2801/c
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; ORGANISM: Homo sapiens
US-09-796-692-2801
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Best Local Similarity 99.3
Matches 285; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 2801
LENGTH: 287
CURRENT APPLICATION NUMBER: US/10/040,862
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
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APPLICATION NUMBER: 60/200,303
FILING DATE: 2000-04-28
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NUMBER: 60/223,378
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Pred. No. 2e-74;
                                         and Methods for the Detection,
al Malignancies
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-2801
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Best Local Similarity
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SOFTWARE: FastSEQ for
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OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: US 60/200,779
OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: US 60/200,999
OR FILING DATE: 2000-05-01
OR APPLICATION NUMBER: US 60/202,084
OR FILING DATE: 2000-05-04
OR APPLICATION NUMBER: US 60/206,201
OR APPLICATION NUMBER: US 60/206,201
OR APPLICATION NUMBER: US 60/206,201
OR APPLICATION NUMBER: US 60/218,950
OR APPLICATION NUMBER: US 60/222,903
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FILING DATE: 2000-08-07
APPLICATION NUMBER: US 09/796,692
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APPLICATION NUMBER: US 60/223,416
FILING DATE: 2000-08-04
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RESULT 20
US-10-57-475B-2801/c

Sequence 2801, Application US/10057475B

Publication No. US20040002068A1

Publication No. US20040002068A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wanng, Aljun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren

APPLICANT: MCNeill, Patricia Dianne
APPLICANT: Corixa Corporation
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US-10-154-884B-2801/c
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
                                                                                                                                                                             Sequence 2801, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 10979
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2801
LENGTH: 287
        APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mennion, Jane
APPLICANT: Corixa Corporation
TIPLE OF INVENTION: Compositions and Methods for the Detection,
TIPLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/154,884B
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APPLICATION NUMBER: US 60/200,303
APPLICATION NUMBER: US 60/200,779
APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
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APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
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FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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Pred. No. 2e-74;
0; Mismatches
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RESULT 22
US-10-764-324-2801/c
; Sequence 2801, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
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SEQ ID NO 2801
LENGTH: 287
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Matter, Marc
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
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PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-04
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
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PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
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ORGANISM: Homo sapiens
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Pred. No. 2e-74;
0; Mismatches
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APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: US/10/040,862 PRIOR FILING DATE: 2001-11-06

APPLICATION NUMBER: US 60/186,126

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GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.

APPLICANT: MAIGHTE, Paul A.

APPLICANT: MANDION, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,545
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US-09-796-692-5724
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Best Local Similarity
Matches 285; Conserv
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LENGTH: 287
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR TLING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
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ORGANISM: Homo sapiens
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PILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,999
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APPLICATION NUMBER: US 60/190,479
FILING DATE: 2000-03-17
APPLICATION NUMBER: US 60/200,545
                       APPLICATION NUMBER: 60/200,303 FILING DATE: 2000-04-28
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PRIOR APPLICATION NUMBER: US 60/190,479
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RESULT 24
US-10-040-862-5724
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US-09-796-692-5724
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Mannion, Jane

APPLICANT: Corixa Corporation

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap:

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-013520US

CURRENT APPLICATION NUMBER: US/10/040,862

CURRENT APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                 Sequence 5724, Application US/10040862
Publication No. US20030078396A1
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Best Local (
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SEQ ID NO 5724
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TYPE:TIM: HOMO SAPIENS
PEATURE:
PEATURE:
NAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: n=A,T,C o
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OR FILING DATE: 2000-08-03
OR APPLICATION NUMBER: 60/223,416
OR FILING DATE: 2000-08-04
OR APPLICATION NUMBER: 60/223,378
OR FILING DATE: 2000-08-07
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FILLING DATE: 2000-05-04
APPLICATION NUMBER: 60/206,201
FILING DATE: 2000-05-22
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ilarity 98.6%;
Conservative
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DS: 9597
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Pred. No. 5.4e~71;
0; Mismatches 3;
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ARPELL APPLICATION PRIOR FILING PRIOR PILING DATE:

PRIOR APPLICATION PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER: US 60,

PRIOR PILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: US 60/72.

VIOR PRILING DATE: 2000-08-07

IOR APPLICATION NUMBER: US 60/72.

VIOR PRILING DATE: 2000-08-07

IOR APPLICATION NUMBER: US 69/796,6.

TOR FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: US 09/796,6.

TOR PILING DATE: 2001-03-01

PRIOR SEQ ID NOS: 10467

WARE: FASTSEQ for Windows Version 3.0

NO ST24

"H: 288

DNA

SM: Homo sapiens

": unsure
(58)

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US-10-057-475B-5724
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Sequence 5724, Application US/10057475B
Publication No. US20040002068A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
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Best Local Similarity
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NAME/KEY: unsure
NAME/KEY: (59)
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OTHER INFORMATION: n=A,T,C
·10-040-862-5724
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APPLICATION NUMBER: US 6
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APPLICANT: Colic:, Batricia Dianne
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
ITILE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT APPLICATION NUMBER: US 60/166,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,709
PRIOR APPLICATION NUMBER: US 60/200,709
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-03
PRIOR PRIOR PRIOR DATE: 2000-08-03
PRIOR PRIOR DATE: 2000-08-03
PRIOR PRIOR DATE: 2000-08-03
PRIOR DATE: 2000-08-04
PRIOR DAT
RESULT 26
US-10-154-884B-5724
; Sequence 5724, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
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LENGTH: 288

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(288)
OTHER INFORMATION: n = 9
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Best Local Similarity
Matches 284; Conserv
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Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Pred. No. 5.4e-71;
0; Mismatches 3
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RESULT 27
US-10-764-324-5724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5724
LENGTH: 288
TYPE: DNA
Sequence 5724, Application US/10764324 Publication No. US20040175739A1 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILLING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILLING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILLING DATE: 2000-04-27
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CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
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APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis

TITLE OF INVENTION: Hematological Malignancies
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APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
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APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
APPLICATION NUMBER: US 60/206,201
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FILING DATE: 2000-04-28
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PRIOR APPLICATION NUMBER: US: 00/186,126
PRIOR APPLICATION NUMBER: US: 60/186,126
PRIOR APPLICATION NUMBER: US: 60/190,479
PRIOR APPLICATION NUMBER: US: 60/200,545
PRIOR PRILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US: 60/200,545
PRIOR APPLICATION NUMBER: US: 60/200,545
PRIOR APPLICATION NUMBER: US: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US: 60/200,779
PRIOR APPLICATION NUMBER: US: 60/200,779
PRIOR APPLICATION NUMBER: US: 60/200,999
PRIOR APPLICATION NUMBER: US: 60/200,084
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NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5724
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: n=A,
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CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Hematological Malignancies
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APPLICANT: Algate, Paul A.
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APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
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                          TCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTTT 538
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Retter, Marc
Corixa Corporation
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milarity 98.6%;
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Pred. No. 5.4e-71;
0; Mismatches 3
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RESULT 29
US-10-094-466-41
; Sequence 41, Application US/10094466
; Publication No. US20030203363A1
; GENERAL INFORMATION:
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Best Local S
Matches 346
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 25411
LENGTH: 527
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: MAP TO AC012678.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.51
OTHER INFORMATION: SWISSPROT HIT: Q61768, EVALUE 1.10e-01
OTHER INFORMATION: NT HIT: AF120995.1, EVALUE 1.30e-01
OTHER INFORMATION: EST_HUMAN HIT: BF744133.1, EVALUE 2.00
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                                                                                                                                 AACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA 601
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Pred. No. 2.5e-60;
0; Mismatches 181;
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 CTGACCGCCAAGTCCCACGGCCGCATCAACCACGTGTTCGGCCCACCTAGCCGACTGCGAC
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; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(584)
US-10-094-466-41
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CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/288,148
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/275,235
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/338,375
PRIOR PILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/275,579
PRIOR APPLICATION NUMBER: 60/275,579
PRIOR APPLICATION NUMBER: 60/335,302
PRIOR PILING DATE: 2001-03-13
PRIOR PILING DATE: 2001-03-13
PRIOR PILING DATE: 2001-03-13
PRIOR PILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/275,601
PRIOR PILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/276,000
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PRIOR FILING DATE: 2001-12-04
PRIOR PELICATION NUMBER: 60/275,579
PRIOR PELICATION NUMBER: 60/275,579
PRIOR APPLICATION NUMBER: 60/275,501
PRIOR APPLICATION NUMBER: 60/275,601
PRIOR APPLICATION NUMBER: 60/276,000
PRIOR FILING DATE: 2001-03-13
PRIOR PELICATION NUMBER: 60/276,000
PRIOR FILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-27
PRIOR PILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.6%;
Best Local Similarity 59.9%;
Matches 347; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatIn 2.1
                                                                                                                                                                                                                                                                                                                                                                                             AGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAAGTT
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CTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAA
                                                                  GTGCTGGCCGGGGCTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGGTCCCCAC
                                                                                                                                     GTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCAC
                                                                                                                                                                                                           CGCTGCCTGGCCATGACGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGC
                                                                                                                                                                                                                                                                      CATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAAT
                                                                                                                                                                                                                                                                                                                                         CGTGGGGACCAGCTGGGCGGTGAGGAGCTGGCGCTGCTGCGGCGCTTCCGCCACCGGGCG
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Pred. No. 2.2e-51;
0; Mismatches 232;
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502
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No:
US-10-416-314-70
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US-10-416-314-70
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PRIOR APPLICATION NUMBER: US 60/249,642
PRIOR FILING DATE: 2000-11-09
PRIOR PELICATION NUMBER: US 60/249,824
PRIOR APPLICATION NUMBER: US 60/252,824
PRIOR PRIOR DATE: 2000-11-21
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR PILING DATE: 2000-12-08
PRIOR PILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/254,305
PRIOR APPLICATION NUMBER: US 60/256,448
Query Match
Best Local Similarity
Matches 347; Conserv
                                                                                                                                                                                                                    SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 70, Application US/10416314
Publication No. US20040082508A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/416,314
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/247,505
PRIOR FILING DATE: 2000-11-08
                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 130
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DUGGAN, Brendan M.
APPLICANT: KAREHT, Stephanie K.
TITLE OF INVENTION: SECRETED PROTEINS
FILE REFERENCE: PI-0287 USN
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                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                    LENGTH: 2108
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YANG, Junming
LAL, Preeti G.
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WARREN, Bridget A.
HONCHELL, Cynthia D.
LU, Dyung Aina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GANDHI, Ameena R.
BAUGHN, Mariah R.
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ISON, Cra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DING,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SANJANWALA, Madhusudan M. THORNTON, Michael B. ELLIOTT, Vicki S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWARNAKAR, Anita
CHAWLA, Narinder K.
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  Conservative
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                  34.6%;
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  0;
                  Score 207.8; DB 1
Pred. No. 4.4e-51;
  Mismatches
                                                                                                   2013095CB1
                                       DB 18;
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  Indels
                                     Length 2108;
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                                                                              APPLICANT: Xue, Aidong J.
APPLICANT: Ma, Yunqing
APPLICANT: Mang, Zhiwei
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Damanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20020150898A1el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791C1P2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT APPLICATION UNMEER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
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US-09-816-828-5
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                SOFTWARE: pt_FL_genes
SEQ ID NO 5
LENGTH: 1188
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tang, Y. Tom
  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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Zhou, Ping
Trich, Ryle
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Asundi, Vinod
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Aidong J.
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502 831 442

562 891

951

651 262 591 202

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RESULT 32
US-10-094-466-43
; Sequence 43, Application US/10094466
; Publication No. US20030203363A1
; GENERAL INFORMATION:
; APPLICANT: SPYTCK et al.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, PO
; TITLE OF INVENTION: AND METHODS OF USING
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-290D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   д
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; LOCATION: (174)..(731)
US-09-816-828-5
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PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/28,148
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR APPLICATION NUMBER: 60/275,235
PRIOR APPLICATION NUMBER: 60/275,235
PRIOR APPLICATION NUMBER: 60/275,235
PRIOR APPLICATION NUMBER: 60/338,375
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Best Local Similarity
Matches 343; Conserv
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/094,466
CURRENT FILING DATE: 2002-03-07
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Pred. No. 1.4e-50;
0; Mismatches 229;
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SEQ ID NO 43

; LENGTH: 619

; TYPE: DNA

; ORGANISM: Homo sapien:

; EBATURE:

; NAME/KEY: CDS

; LOCATION: (2)...(566)

US-10-094-466-43
                RESULT 33
US-10-764-420-2116
; Sequence 2116, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/235,302
PRIOR FILING DATE: 2001-0-31
PRIOR FILING DATE: 2001-03-13
PRIOR PILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/275,601
PRIOR APPLICATION NUMBER: 60/276,000
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/277,338
PRIOR FILING DATE: 2001-03-09
PRIOR PRIOR FILING DATE: 2001-03-09
PRIOR PRIOR PRIOR SEQ ID NOS: 114
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Best Local Similarity
Matches 339; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   364
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                                                                                                                                                            GATGCTGGACGAGGGCAGCCTCTGA
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                                                                                                                                                                                                                                                                                                                     CCACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGACTGCGACTTCCTGGCTGCGCT
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543

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363 456 423

483

396

336

123 216 183 276 243

303

63 156

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APPLICANT: Tan, Yejun
APPLICANT: Dai, Hongyue
ITITLE OF INVENTION: Methods For Determining Whether An Agent
ITITLE OF INVENTION: Possesses A Defined Biological Activity
FILE REFERENCE: ROSA122057
CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR APPLICATION NUMBER: US 60/474,413
PRIOR FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: US 60/474,413
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 3683
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 2116
LENGTH: 1389
TYPE: DNA
ORGANISM: Mus musculus
PEATURE:
NAME/KEY: misc_feature
LOCATION: 80
TYPE: DNA
ORGANISM: Misc_feature
LOCATION: 80
TYPE: DNA
ORGANISM: Misc_feature
                                                        RESULT 34
US-09-822-849A-81
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     Sequence 81, Application US/09822849A Patent No. US20020045170A1 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                 ATGGACGGGTTAATAATGTCTTTGATCATTTTTTCAGATTTGTGAATTTTTTGGCTGCCTTGT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAGAAGATCTTGGGTA
                                                                                                                                                                                                                                                                                    ACGGCCGCATCAATCACATCTTCAGTCACTTTGCCAATGGTGACTTCCTGGCCGCGCTGT
                                                                                                                                                                                                                                                                                                                                                             TGCTGGAGTGCAGGGACCTGTTGCACCAGGCTATTGGCCCGCACCTCACTGCCAAGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCCCTCAGCTTCCACCAGGTAGACTTCACCTTTGACCGGCGTGTGCTGGCCACTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGATCA 218
                                                                                                                                                                    TGTTGGATGAAGAGAACATATGA 601
                                                                                                                                                                                                         ACAGCCCAGCAGAGCCCTACCGGAGCCATCTGTGCCGCATCTGTGATGGCCTCGGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                TANATGAATGCAGAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCAATGAGCTGGCCCAGCTGCAGCGGTTCCGGGGCCGCCGTCCGCCAACCTGGCCATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATGGACACCTTCAGCACGAAGAGCCTGGCCCTGCAGGCCCAGAAGAAAGTCCTCAGCA 141
                                                                                                                                   TGTTGGACGAGGGTGGCATCTGA
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59.7%;
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Pred. No. 8.6e-49;
0; Mismatches 227;
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; TYPE: DNA
; ORGANISM: Homo &
US-09-822-849A-81
RESULT 35
US-10-363-374-15
; Sequence 15, Application US/10363374
; Publication No. US20050048483A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
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Best Local Similarity
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: Clark, Hilary
: Fechtel, Kim
                                                                                                                                                                                                                                                                                                             CCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                              CCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTG
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                                                                                                                                   TCAGGAAGCTGCTAGACGAAGGGAAGCTCTGA
                                                                                                                                                                    TCAACAAAATGTTGGATGAAGAGAACATATGA 601
                                                                                                                                                                                                         CGGCCCTCTATGGGCCT-----GACTTCACTCAGCACCTTGGCAAGATCTGTGACGGAC
                                                                                                                                                                                                                                           CTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTA
                                                                                                                                                                                                                                                                                  CCAAGTCACATGGCCGCATCCGCCACGTGTTTGATCACTTCTCTGACCCCAGGTCTGCTCA
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Gulukota, Kamalakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Graham, James R.
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Pred. No. 1.7e-43;
0; Mismatches 230
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Length 1113; Indels

6;

Gaps

111

171

149

449

411

509 471

531

329

351

269

291

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RESULT 36
US-10-302-172-537
; Sequence 537, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
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Best Local Similarity 58.7%;
Matches 336; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (100)..(651)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (100)..(180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2 SEQ ID NO 15
APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Drmanac, Radoj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Su, Bric
APPLICANT: Wang, He
TITLE OF INVENTION: NOVEL SECRETED PROTEI:
FILE REFERENCE: X13020
CURRENT APPLICATION NUMBER: US/10/363,374
CURRENT FILING DATE: 2003-02-27
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                           TCAGGAAGCTGCTAGACGAAGGGAAGCTCTGA
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Pred. No. 1.7e-43;
0; Mismatches 230;
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CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR PILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEO ID NOS: 950
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 537
LENGTH: 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids TITLE OF INVENTION: Polypeptides FILE REFERENCE: 803 1CNCP CURRENT APPLICATION NUMBER: US/10/302,172
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TCAGGAAGCTGCTAGACGAAGGGAAGCTCTGA
                                                                   CGGCCCTCTATGGGCCT-----GACTTCACTCAGCACCTTGGCAAGATCTGTGACGGAC
                                                                                        CTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTA 569
                                                                                                                                      CCAAGTCACATGGCCGCATCCGCCACGTGTTTGATCACTTCTCTGACCCAGGTCTGCTCA
                                                                                                                                                                                                          CTGGCCTGCTGACCGAGTGCCGGGATGTGCTGCTAGAGTTGGTGGAACACCACCTCACGC
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Pred. No. 1.7e-43;
0; Mismatches 230;
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RESULT 37
US-10-959-539-59
; Sequence 59, Application US/10959539
; Publication No. US20050048623A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.

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US-10-959-539-59
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Best Local Similarity
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LENGTH: 1268
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CURRENT FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US/10/031,915
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/145,075; 60/153,129; 60/164,647
PRIOR PILING DATE: 1999-07-21; 1999-09-08; 1999-11-10
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHAH, PUTVI
TITLE OF INVENTION: CELL CYCLE AND PROLIFERATION PROTEINS
FILE REFERENCE: PF-0722 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Incyte ID No: 1558289CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
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570 TCAACAAAATGTTGGATGAAGAGAACATATGA 601
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                                                                                                                                                                                                                                                             CTGGCCTGCTGACCGAGTGCCGGGATGTGCTGCTAGAGTTGGTGGAACACCACCTCACGC
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                                                                                                                       CTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTA 569
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LU, Dyung Aina M.
BAUGHN, Mariah R.
PATTERSON, Chandra
                                                                                                                                                                    CCAAGTCACATGGCCGCATCCGCCACGTGTTTGATCACTTCTCTGACCCAGGTCTGCTCA
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BANDMAN, Olga
AZIMZAI, Yalda
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Pred. No. 1.8e-43;
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                                                                                              APPLICANT: Hyeeq, Inc.
APPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRA
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
INUMBER OF SEQ ID NOS: 38054
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35521
LENGTH: 422
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-918-995-35521
; Sequence 35521, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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                                                                        ; ORGANISM: Homo sapiens US-09-918-995-35521
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US-10-029-386-9211
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APPLICANT: Penn, Sharron G.
APPLICANT: Renk, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 9211
Query Match
Best Local Similarity
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Best Local Similarity
Matches 169; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AC035144.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: EST_HUMAN HIT: BG178783.1, EVALUE 0.00e+00
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTT
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Pred. No. 1.2e-39;
  Score 128.4; DB 10;
Pred. No. 1.1e-27;
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CDNA LIBRARIES
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RESULT 41
US-10-191-803-330/c
; Sequence 330, Application US/10191803
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APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
TITLE OF INVENTION: LIVESTOCK
FILE REFERENCE: MMI1110-2
CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SEQ ID NO 232
LENGTH: 565
TYPE: DNA
ORGANISM: Chicken 19866894084041_1
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US-10-972-079-232
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APPLICANT:
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KERR, Richard
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Pred. No. 1.3e-13;
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                          APPLICANT: Algare, Paul A.

APPLICANT: Algare, Paul A.

APPLICANT: Mannion, Jane

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAC

ITITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796,692

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/200,099

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/200,094

PRIOR PILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/206,201

PRIOR APPLICATION NUMBER: 60/206,201
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APPLICANT: ELASHOFF, Michael

FIITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling

FILE REFERENCE: 44921-5090US

CURRENT APPLICATION NUMBER: US/10/191,803

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US 60/303,819

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/305,623

PRIOR FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US 60/369,351

PRIOR FILING DATE: 2002-04-03

PRIOR FILING DATE: 2002-04-03

PRIOR APPLICATION NUMBER: US 60/377,611

PRIOR APPLICATION NUMBER: US 60/377,611
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US-09-796-692-4917/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 330
LENGTH: 493
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APPLICANT: MENDRICK, Don
APPLICANT: PORTER, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4917, Application US/09796692 Publication No. US20020198362A1
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NUMBER OF SEQ ID NOS: 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAACAAAATGTTGGATGAAGAGAACATATGA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAACAAAATGTTGGATGAAGAGAAACATATGA 601
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Pred. No. 7.3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mantion, Jane
APPLICANT: Mention, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-040-862-4917/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/190,479 PRIOR FILING DATE: 2000-03-17
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (77)
OTHER INFORMATION: n=A,T,C or
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ORGANISM: Homo sapiens
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les 63; Conserv
                                      FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
FILING DATE: 2000-08-03
APPLICATION NUMBER: US 60/223,416
FILING DATE: 2000-08-04
APPLICATION NUMBER: US 60/223,378
                                                                                                                                                            APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
APPLICATION NUMBER: US 60/218,950
                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/200,999
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/200,779 FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/200,303
FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/200,545 FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                 FILING DATE: 2000-05-01
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NUMBER: US 09/796,692
                   2000-08-07
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100.0%; Pro
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Pred. No.
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; LOCATION: (77)
; OTHER INFORMATION: n=A,T,C
US-10-040-862-4917
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                                                                                            SOFTWARE: Fas
SEQ ID NO 4917
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Best Local Similarity
Matches 63; Conserv
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                                                                                                                                  Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 10979
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 014058-014402ŬS
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10467
                                                                                                                                                                       PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaiger, Alexander
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                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT:
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                            ENGTH: 538
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                                                                                                                                                                                     APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/200,999
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/200,779
                                                                                                                                                                                                                                              FILING DATE: 2000-05-22
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/206,201
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mannion, Jane
Clapper, Jonathan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McNeill, Patricia Dianne
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APPLICANT: Admics, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
CURRENT PLILORION NUMBER: US/10/154,884B
CURRENT APPLICATION NUMBER: US 60/186,126
FRIOR FILLING DATE: 2000-03-01
PRIOR FILLING DATE: 2000-03-01
PRIOR FILLING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILLING DATE: 2000-04-28
PRIOR FILLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILLING DATE: 2000-05-02
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FEATURE:
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FORMATION: (1)...(538)
CTHER INFORMATION: n = 9, a, c or t
US-10-154-884B-4917
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Sequence 4917, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = g, a, c
US-10-057-475B-4917
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                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4917
LENGTH: 538
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 11290 SOFTWARE: FastSEQ for Windows Version 3.0
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Qy 599 TGA 601 ||| Db 478 TGA 476

Search completed: July 28, 2005, 19:13:31 Job time: 593 secs

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Result
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J 175503. Y

HX405197

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EST18330

HP228279

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AUTHORS
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CF593784
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Best Local Similarity
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Conteact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: Capabs-remail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

CDNA Library Preparation: Michael J. Brownstein (NHGRI) with he and advice from Piero Carninci (RIKEN)

and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.linl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 806)
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EST.
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AGENCOURT 15624053 NIH MGC 147 Homo
IMAGE:30528465 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                     CTTCAGCGTCCCGGCGCCGTCGCGCCACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                                                                                                                                     CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                           ANAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                   AAAACCTGGCCGTTCAGGCACAAAAGAAGTTCTTGGGTAAAATGGTGTCCAAATCCATCG
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Location/Qualifiers
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fMAGE:30528465"
/tissue_type="Human Placenta"
/lab_host="DH10B_TonA"
                                                                                                                                                                                                                                                                                                         /clone lib="NIH MGC 147"
/note=Torgan: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
a NIH_MGC library."
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BP277360
AU136721
                                                                                                                                                                                                                             Score 588.4; DB 7;
Pred. No. 3.9e-152;
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AU136721 AU136721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 bp mRNA linear ES' AGENCOURT 15178772 NIH MGC 192 Homo sapiens cDNA clone IMAGE:305T2832 5', mRNA sequence.
CF272384
CF2722384.1 GI:33628296
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 920)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
                                                                                                                                                                       http://image.llnl.gov
Plate: NDAM573 row: m column:
                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                               National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                               cDNA Library Preparation: Agencourt
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                   quality sequence stop: 598 Location/Qualifiers
/clone="IMAGE:30512832"
/tissue_type="Brain glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 600;
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                                                                                        AACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAAGAACATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_192"
/note="Vector: pExpress1; Site_1: Smal; Site_2: Not1; The library was constructed by reverse transcription of 1 ug mRNA using the oligo dT primer GCGGCCGCC(T)20 and an RNaseH + MMLV reverse transcriptase. Second strand synthesis was carried out by standard methods. The cDNA was size selected by agarose gel for > 1.2 kb, digested with Not I and directionally cloned into the vector Express-1 at the Smal/NotI sites. DNA from the primary library was used for in vitro transcription from the T7 promoter to produce biotinylated RNA transcripts. These biotinylated transcripts, along with blocking oligos to the poly-A, multiple cloning site and primer regions, were hybridized with single stranded circles produced by phagmeid production from the primary library to a Cot value of 10-20. Strepavidin/phenol extraction was utilized to remove DNA:RNA hybrids leaving un-hybridized single stranded circles which were repaired by primer extension and transformed back into E. coli resulting in the normalized library. Average insert size 2.0 kb 3' linker/adaptor sequence GCGGCCCC(T)20. This libary was constructed by Agencourt Biosccience."
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Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 737 Std Error: 0.00.
Location/Qualifiers
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Contact: Brandenberger R
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S.,
Lebkowski, J and Stanton, L.W.
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                                                                                        TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG
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/note="oligo dT primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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line"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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IMAGE:30347855 5', mRNA sequence.
CB990165
CB990165.1 GI:30284685
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: NDAM389 row: j column: 24
High quality sequence stop: 635.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 780)
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National Institutes of Health, Mammalian
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AAAACCTGGCCGTTCAGGCACAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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                                                                                                                                  Conservative
                                                                                                                                                                                                                /note="Organ: placenta; Vector: pBluescriptR; Site_1: all-XhoI; Site_2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This a NIH_MGC library."
                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Human Placenta"
/lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="NIH_MGC_147"
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                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 813)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLMM11437 row: 1 column: 07 High quality sequence stop: 809.
Location/Qualifiers
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/clone="IMAGE:5175702"
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Query Match
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/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
clestroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
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AACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATAT
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Rogan: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
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/clone="IMAGE:6153217"
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|mol_type="mRNA"
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Pred. No. 2.1e-151;
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ACCESSION VERSION KEYWORDS

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599 601 539 541 479 481 419 421 359 361

RESULT 6 BQ424670 LOCUS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11481 row: j column: 18
High quality sequence stop: 813.
Location/Qualifiers
1 876
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[ (bases 1 to 876)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                    GGGAGTACACCCAAAACAAGAAGGAGGGCAGAGAAGATCATCAAGAAACCTCATCAAGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5192561"
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Pred. No. 3.5e-148;
0; Mismatches 3;
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KEYWORDS
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Madiater
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17000532623591 GRN_ES Homo
CN305327
CN305327.1 GI:47321741
                                                                                                                                                                                                                                                                  Geron Corporation
230 Constitution Drive,
Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I (bases 1 to 712)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J.
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 Conservative
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Length: 712 Std Error:
Location/Qualifiers
                                                                      /clone lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                               tissue_type="embryonic stem cells,
             93.9%;
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Score 564.4; DB 7;
Pred. No. 1.8e-145;
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                                                                                                          Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 9157 EWRY cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 9157 EWRY cedex - FRANCE Email: segrat@genoscope.cns.fr, Web : www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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AL549492 Homo sapiens PLACENTA COT 25 NORMALIZED Clone CSODI044YG13 5-PRIME, mRNA sequence.
AL549492
AL549492
AL549492.3 GI:45749887
EST.
                                                                                                                                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replacements
                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO44ADO7QPl&c=3485.f. Location/Qualifiers
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1 (bases 1 to 718)
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI--ligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/clone="CS0DI044YG13"
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can
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http://image.llnl.gov
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TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACA
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/clone lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adm Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCGCACATG-dT(10)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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/tissue_type="Pooled"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:31065417.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and ECGR V sites of the pCMVSPRT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
                                                                                                                                                                                                                                       GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
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                                                                    TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                                                                                                                                                                                                                                                                           TGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
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/db_xref="taxon:9606"
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Pred. No. 1.9e-145;
0; Mismatches 1;
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AGENCOURT 6715690 NIH_MGC_120
5', mRNA sequence.
BM919223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNE at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1055)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
Plate: LLAM12776 row: d column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 677.
Location/Qualifiers
                     Conservative
                                                                                                           /clone libe WIH MGC 120"
/clone libe WIH MGC 120"
/note=Torgan: pooled pancreas and spleen; Vector:
/note=Torgan: pooled pancreas and spleen; Vector:
pcWV-SPORT6; Site 1: Not1; Site 2: ECGRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5748442"
                                                                                                                                                                                                                                                                                                                            lab_host="DH10B"
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                                 Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                   Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished Contact: Feng Liang Email: fliang@lifetech
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     Location/Qualifiers
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1 (bases 1 to 1733)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
 Faraday Avenue
2 (bases 1 to
                  Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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CR615621.1 GI:50496428
HTC; CNSLT_CDNA.
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/db_xref="taxon:9606"
/clone="CSUDIO57YA07"
/tissue_type="Placenta Co-
/plasmid="pCMVSPORT_6"
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CR615131
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Direct Submitsion

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr -

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
                      AAATGTTGGATGAAGAGAACATATGA
                                                                                 TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGA
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AAATGTTGGATGAAGAGAACATATGA
                                                                                                                                                                          CACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODCO24YA33"
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1754 bp (CS0DI081YO11

mRNA linear L of Placenta Cot

25-normalized HTC 21-JUL-2004

linear

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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Faraday Avenue
2 (bases 1 to 1754)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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1 (bases 1 to 1754)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT)
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    AAATGTTGGATGAAGAGAACATATGA 601
                                                                                                                                                           CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Pred. No. 2.2e-145;
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336 TGACCGTGGTCAGTTTCCAGCAGGGGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                                      181 TCATCAAGAACCTCATCAAGACAGTTATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA with a NotI and cloned
into the NotI and EcoR V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 885)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDM libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31272274.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL550457 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens Clone CSODI057YA07 5-PRIME, mRNA sequence.

AL550457
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO57AA04QP1&c=3485.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAAGTTCATCAGCTTGCTA
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/clone="CS0DI057YA07"
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Pred. No. 5.2e-145;
0; Mismatches 2;
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-101go(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Feb 15, 2001 this sequence version replaced Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1045)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone CS0DI081YO11 5-PRIME, mRNA sequence.
AL554168
AL554168.3 GI:45858929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.genoscope.cns.fr/cdna?s=CS0DI081AH06QP1&c=3485.f
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                             GTAAAATGGTGTCCAAATCCATCGCCACCACCTAATAGACGACACAAGTAGTGAGGTGC
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                                                                                                              TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAGAAGATCTTGG
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      GTAAAATGGTGTCCAAATCCATCGCCACCATTAATAGACGACACAAGTGGTGAGGTGC
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                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                   /tissue_type="PIACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI081Y011"
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                                                                                                                                                                                    93.6%;
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AGENCOURT 13618130 NIH MGC 148 Homo sapiens
IMAGE:30337918 5', mRNA sequence.
CB991862
                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with l
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 785)
                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAM363 row: 1 column: 23
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                                                                                                                                                                                                       quality sequence stop: 629.
Location/Qualifiers
/organism="Homo sapiens"
/mol type="mRNA"
/mb xref="taxon:9606"
/clone="IMAGE:30337918"
/tissue_type="pre-eclamptic placenta"
/lab host="DH10B TonA"
/clone_lib="NJH MGC_148"
/note="Organ: placenta; Vector: pBluescall-XhoI; Site_2: BamH; Library is olig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (human)
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Best Local Similarity
Matches 583; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                        578
Eukaryota; Metazoa; Chordata; C: Mammalia; Eutheria; Primates; C: 1 (bases 1 to 779)
Li,W.B., Gruber,C., Jessee,J. an Full-length CDNA libraries and I Unpublished (2001)
On Feb 15, 2001 this sequence ve Contact: Genoscope
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AL542926 Homo sapiens PL
5-PRIME, mRNA sequence.
AL542926
AL542926 3 GI:45718495
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Pred. No. 2.3e-144;
0; Mismatches 1;
                                                        and
                version replaced gi:30548565
                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                       and Polayes, D.
                                                      normalization
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr prime ist strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence belongs to sequence cluster 3485.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE013CE09QP1&c=3485.f. Location/Qualifiers
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                     AAATGTTGGATGAAGAGAACATATGA
                                                                      TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                         TGTATAATCCTTTTTGGGAATTTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                         CACATGGACGGGTTAATAATGTGTTTGAYCATTTTTCAGATTGTGAATTTTTGGCTGCCT
                                                                                                                                                                      CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
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/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone="Vector: pCMVSPORT 6; 1st strand cDNA was primed in the NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and ECORV sites of the pCMVSPORT 6 vector.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1:1e-143;
2; Mismatches 2;
566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKF2p469E1232) is available the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR548728
CR548728.1 GI:50242352
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This is the 5' sequence of the clone insert Clone from S. Wiemann
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s wiemann@dkfz-heidelberg.de; sequenced by Qiagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Fobo, G., Han, M. and Wiemann, S. Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Unpublished (2004)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 779)
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                                                                                          TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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                               TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2:
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/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9600"
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Pongo pygmaeus cDNA clone
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 559)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31283006.

Contact: Genoscope
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Homo sapiens cDNA clone
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GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
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                                                                                   GTAAAATGGTGTCCAAATCCATCGCCACCACCATAATAGACGACACAAGTAGTGAGGTGC
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                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="traxon:9606"
/clone="CSODJ015YH04"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 8.8e-143;
7; Mismatches 1;
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                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11457 row: k column: 04
High quality sequence stop: 869.
High quality sequence stop: 869.
                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI759027.1 GI:15750605
EST.
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603042814F1 NIH_MGC_116
                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 893)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (human)
           /clone lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach, Vector:
/note="Organ: pooled colon, kidney, stomach, Vector:
pCMV-SPORTG, Site 1: Not1; Site 2: ECORV (destroyed);
source anonymous pool of 3 colons, age 26 yo male, 49
female, 71 yo male colon; 46 yo male kidney, and pool
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site
destroyed upon cloning).
                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183355"
                                                                                                                                                   organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                              ocation/Qualifiers
                                                                                                             host="DH10B"
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Average insert size 1.4 kb
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Similarity
AAATGTTGGATGAAGAGAACATATGA
                                                                                                            TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGATCAACA
                                                                                                                                                                      CACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAA-TTTTGGCTGCCT
                                                                                                                                                                                         CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                                                                                                                                      TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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                                                                                  TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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CUS CN648259
ILLUVIGEN MCQ 30108 Katze MMPB Macaca mulatta cDNA clone IBIUW:6795
5' similar to Bases 72.to 998 highly similar to human TNFAIP8
(Hs.17839), mRNA sequence.
CCESSION CN648259
CCASSION CN648259.1 GI:47161702
EXT.
WACACA mulatta (rhesus monkey)
Macaca mulatta (rhesus monkey)
Macaca mulatta Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (Dases 1 to 998)
AUTHORS
KALZe,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE
Large-scale Rhesus Macaque cDNA Sequencing
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
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Best Local S
Matches 555
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634
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                AAATGTTGGATGAAGAGAACATATGA
                                                                      TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                            CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_Stage="adult"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MMPB"
/note="Vector: UnI-ZAP XR; Site_1: EcoR I; Site_2: Xho I
Created from Stratagene ZAP-cDNA Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit
(Catalog #200450)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="blood"
/cell_type="PBMC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IBIUW:6795"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Indian"
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Pred. No. 5.4e-141;
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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Best Local Similarity
Matches 562; Conserv
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JOURNAL
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Hellx Research Institute
1522-3 Yana, Kisarazu, Chi
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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AU135377
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HRI human cDNA project; 5'. & 3'.end one pass sequencing: Helix
Research Institute; cDtA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Yamamoto, J., Wakamatsu, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 816)
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                           TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                      TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                   TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1001920"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="placenta"
/clone_lib="PLACE1"
/note="Vector: pME18SFL3"
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98.9%;
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sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 547.6;
Pred. No. 8.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 580)

1 (bases 1 to 580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jag
Email: ysuzuki@ims_u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S. Sequence comparison of human mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
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BP302623 Sugano cDNA library,
MPE06324, mRNA sequence.
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                                                                                                                                                                               GACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGAIGAGCTAGC
                                                                                                                                                                                                                                                           GACCAGGGAGTACACCCAAAAACAAGAAGGAGGAGGAGAAGATCATCAAGAACCTCATCAA
                                                                                                                                                                                                                                                                                                              CATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                TTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATC
                        ATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCA
                                                                                                                                                         GACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGC
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MPE06324"
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|e_lib="Sugano cDNA library, macrophage"
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macrophage Homo sapiens cDNA
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Bridocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                     Seq |
                                                                                                                                                                                                                                                                                                                                                                                      Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq.primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA843219 596 bp mRNA linear EST 13-DEC-2002 ir55c03.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6548934 5' similar to TR:095379 095379 MDC-3.13 ISOFORM 2. [2] TR:Q9UP47 ;,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MA 02138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: .
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617-495-8557
        /tissue type="Purified pancreatic islet"
/lab host="PH10B"
/clone_lib="HR85 islet"
/clone_rib="R85 islet"
/clone_rib="R85 islet"
/note="Forgan: Pancreas; Vector: pBluescript SK(-); Site_1:
/note; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size_-1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab); Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2892."
                                                                                                                                                                                                                                                   clone="IMAGE:6548934"
                                                                                                                                                                                                                                                                         db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                      mol_type="mRNA"
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   Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Ist strand cDNA was primed with a NotI-oligo(GT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                            BX405197
BX405197.2
                                                                                                                                                                                                                                                                 BX405197 834 bp mRNA
BX405197 Homo sapiens T CELLS (JURKAT CELL
clone CS0DH001YB17 5-PRIME, mRNA sequence.
                                                                                                            On May 15, 2003 this sequence version replaced gi:30762567. Contact: Genoscope
                                                                                                                                           Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 834)
                                                                                                                                                                                                                                   EST.
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                                    Homo sapiens (human)
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Pred. No. 2.2e-139;
0; Mismatches 1;
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AGENCOURT 14360208 NIH MGC_191 Homo sapiens IMAGE:30410510 5', mRNĀ sequence. CD520304 GI:31452022 EST. Homo sapiens (human)
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36 TGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
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TTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAAC
                           TTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAAC
                                                                                            TSACATGGACGGGTTAATGATGTTTTGATCATTTTTTGAGATTGTGAATGTTTTGGCTGCG
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/db xref="taxon:9606"
/clone="CSDDH001YB17"
/clsue_type="T CELLS (JURKAT CELL LINE)
/cell_line="JURKAT CELL LINE"
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Pred. No. 2.7e-138;
5; Mismatches 9;
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E: Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NCM200 row: m column: 15
  396
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAGAAGTCTTGG
                                                                                                                                                                                                                                            TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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                                                                   TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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/clone="MAGE:30410510"
/tissue_type="Pooled"
/tissue_type="Pooled"
/tab_host="DH10B (TI phage-resistant)"
/clone lib="WIH MCC_191"
/clone lib="WIH MCC_191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggccgctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CATCTAGAGGCCGACATAG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert. size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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651 DongFeng Road East,
Tel: 86-1380-9770-743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: YiXin Zeng
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Unpublished (2003)
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1 (bases 1 to 622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: yxzeng@gzsums.edu.
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                   TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAAGTTCATCAGCTTGCTA
                                                             TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                               TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                                                                                            TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGAGAAGA
                                                                                                                                                                                   GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
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human nasopharynx Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="normal nasopharynx"
/clone_Tib="human nasopharynx"
/pote="BSTs generated from a normal nasopharynx cDNA
library from southern Chinese"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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100.0%;
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Pred. No. 7e-138;
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CATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCC 353	AGACAGTCATCAAGCTGGCCATTCTTATAGGAATAATCAGTTTAATCAAGATGAGCTAG 293	TGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCA 233	CCATCGCCACCACCATAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAG 173	ATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAAT 113	/ Match 89.0%; Score 535; DB 5; Length 580; Local Similarity 99.6%; Pred. No. 2.5e-137; nes 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	/clone_ilb="Sugano_cDNA_library, dermoid_cancer" /note="dermoid_cancer" FEATURES	-	TITLE Shirokanedai, Minatoku, Tokyo 108-8639, Japan ysuzuki@ims.u-tokyo.ac.jp. Location/Qualifiers 1580	= 11	ACCESSION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; VERSION Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 580) CCESSION EXEMPLES ACCESSION EXEMPLES ACC	GI:52101189 (human)	Qy BP228279 Sugano cDNA library, dermoid cancer Homo sapiens cDNA Clone DMC08045 mBNA someone	TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAACTATGTGATGGTATCA 572	CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT 515		4 3 9
60 AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG	1 CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTAATTCCA 	y Match 88.8%; Local Similarity 98.8%; hes 569; Conservative	rrom mES cell line H/ (p29) maintained in reeder-Tree conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."	/cissue types emilityonic stem ceri, mitogen-treated hass cell line H7" /clone lib="GRN_PRENEU" /note="oligo dT_primed, full-length	•	5	Geron Corporation 230 Constitution Drive, Menlo P Tel: 650 473 8658 Fax: 650 473 7760		3	z	ON	594 ACATATGA 601 540 ACATATGA 547	534 ATTITAAACCCCACTIACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGA 	474 ATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGA	414 AGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATA	240 CATTGATGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCC 354 ATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGTTAAATGAATG

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TITLE
JOURNAL
COMMENT
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CV023086
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Seg primer: Actource start: 104 High quality sequence start: 104
                                 FORWARD: ATGCACTCCGAAGCAGAAGAATCCAA
BACKWARD: CATATGTTCTCTTCATCCAACATT
INSERT Length: 566 Std Error: 21.00
Plate: 11075 row: 05 column: F
CTGCCGTCGTTCTTACAACGTCGTGACTGGGAAAAC
Std primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAAC
                                                                                                                                                                                                         Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, E
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                           Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press
                                                                                                                                                   Email: Marc_Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned results from a PCR_reaction_using an MGC full-length cDNA as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CV023086 566 bp mRNA linear EST 20-AU 5463 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC007014, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 566)
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AUTHORS
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   Poustka,A.,
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Pongo pygmaeus (orangutan)
Pongo pygmaeus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pongo.
1 (bases 1 to 707)
                                                                                                                                                                       DKFZp469E2119_r1 469 (synonym: DKFZp469E2119_5', mRNA sequence CR557522
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/clone_Tib="Full Length cDNA from the Mammalian
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/mol_type="mRNA"
/db_xref="taxon:9606"
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0; Mismatches 1;
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Albert, R., Moosmayer, P.,

Schupp, I.,

Wellenreuther, R.,

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RESULT 34
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LOCUS
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Pongo pygmaeus mRNA (Unpublished (2004)
 CK903031
ir55c03.x5 l
similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469E2119
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/tissue_type="kidney"
/dev stage="adult"
/lab host "DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: Sfila;
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/mol_type="mRNA"
/db_xref="taxon:9600"
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Location/Qualifiers
572 bp mRNA linear EST 11-MAR-2004 HR85 islet Homo sapiens cDNA clone IMAGE:6548934 3' TR:095379 MDC-3.13 ISOFORM 2. [2] TR:Q9UP47 ;,
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Pred. No. 4.3e-136;
0; Mismatches 4;
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CK903031.1 GI
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Contact: Douglas Melton, Klaus H. Kaestner, a ....
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Harvard University, and Cellular Biology, 7 Divinity P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 572)

1 (Dases 1 to 572)

Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D., Welton,D., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenaes,M., Gibbons,M., Ritter,E., Ronko,I., Bennett,J., Cardenaes,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Good hit to opposite strand read. . MOUSE-PANCREAS VERIFICATION
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Other_ESTs: ir55c03.yl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-Harvard Pancreas EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                      AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                                                                                                                                                                                                                                                        CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                                             GGGAGTACACCCAAAACAAGAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                                                                                                                                                                        CTTCAGCGTCCCGGCGCCGTCGCGCCACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
                                                           GGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                     CCACCACCTTAATAGACGACACAAGTAGTGAGGAGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                           CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                                                                              AAAACCTGGCCGTTCAGGCACAAAAGAACTCTTGGGTAAAATGGTGTCCAAATCCATCG
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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ead is a 3' RESEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=Torgan: Pancreas; Vector: pBluescript SK(-); Site_1: Not1; Site_2: KhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:6548934"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="HR85 islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 6.8e-136;
0; Mismatches 2;
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Best Local S
Matches 533
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B: 1 (bases 1 to 697)

S: Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Song,H., Gu,Y., Yang,Y., Jia,J., Fu,G., Ren,S., Zhong,M.; Lu,G., Cheng,Z., and Han,Z.

Lu,G., Cheng,Z. and Han,Z.

Homo sapiens cDNA DCB clones

Lunpublished (2000)

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J51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Tel: 86-21-50801919 (ex.45)
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AV713586 DCB Homo sapier
AV713586
AV713586.1 GI:10795103
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                                                                  TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG
              GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCCCACTTACAAAAA 556
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                                                     TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
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                                                                                                                                                                                                                                                                                                                                         clone
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                       hanzg@chgc.sh.cn
lone is available at CHGC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCB Homo sapiens
                                                                                                                                                                           /note="Vector: pTriplEx2; Site_1:
                                                                                                                                                                                                          /cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBBBB11"
                                                                                                                                                                                             clone_lib="DCB"
                                                                                                                                                                                                                                                                                                             . .697
                                                                                                                      88.1%;
98.9%;
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Pred. No. 9.3e-136;
0; Mismatches 6;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate://image.llnl.gov p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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602506586F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4603917 5',
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Location/Qualifiers
/organism="Homo sapiens"
/mol type="mrNA"
/mb xref="taxon:9606"
/db xref="taxon:9606"
/clome="IMAGE:4603917"
/clome="IMAGE:4603917"
/lab host="DH10B (T1 phage-resistant)"
/lab host="DH10B (T1 phage-resistant)"
/clome lib="NIH MGC_79"
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by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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RESULT 37
CR771358
LOCUS
DEFINITION
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                                                                                                             SOURCE
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VERSION
KEYWORDS
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                                                                                                                                                                       CR771358

DKFZp469I0535_rl 469 (synonym: DKFZp469I0535_r', mRNA sequence
Pongo pygmaeus mRNA
Unpublished (2004)
Contact: MIPS
                                                                                   Pongo pygmaeus (orangutan)
Pongo pygmaeus
Pongo pygmaeus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                    CR771358.1 GI:52614631
CR771358.1 EST.
                                              Poustka, A., Albert, R., Moosma, Mewes, H.W., Weil, B., Amid, C.,
                                      Wiemann,S
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97.7%;
                        (Poustka, A.,
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Pred. No. 3e-1:
0; Mismatches
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                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pongo.
                                              yer,P., Schupp,I., Wellenreuther,R.,
Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                   pkid1) Po
                       Albert, R., Moosmayer, P.,
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BG534704 685 bp mRNA line 602553867F1 NIH_MGC_77 Homo sapiens cDNA clone mRNA sequence.
BG534704

linear EST 03-A one IMAGE:4663672

EST 03-APR-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp46910535 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                            AAATG
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                                                                                                                         TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTAC-AAAACTATGTGATGGTATCAACA
                                                                                                                                             TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pongo pygmaeus"
/mol type="mRNA"
/db_xref="taxon:9600"
/clone="bKrZpA6910535"
/tissue_type="kidney"
/dev stage="adult"
/lab_host="bH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Wector: pSport1_Sfi; Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              GACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGATCATCAAGAACCTCATCAA
GATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAA
                   GATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAA 474
                                                                                                                                                                                                     GACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGC 294
                                                                                                                                                                                                                                                                                                         CATCGCCACCATAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGT 120
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                                                                                                                       ATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCA
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                                                                                                                                                                                  GACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC High quality sequence start: 101 High quality sequence stop: 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 593 Std Error: 7
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA
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1 (Dases 1 to 593)

Rual, J.F., Hirozane Kishikawa, T., Hao, T., Bertin, N., Li, S., Rual, J.F., Hirozane Kishikawa, T., Hao, T., Bertin, N., Li, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: ATGCACTCCGAAGCAGAAGAATCCAA
BACKWARD: CATATGTTCTCTTCATCCAACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Marc_Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry or
results from a PCR reaction using an MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 617 632 5180 Fax: 617 632 5739
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                    /note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gene Collection; into pDoNR223 Donor vector. Reference: MGC (My Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                                                                                                                                                                        Collection"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mtNA"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:51485291
99(26), 16899-16903"
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Mammalian Gene Collection Homo
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C full-length
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Query Match
Best Local Similarity
Matches 547; Conserv

86.4%; ilarity 98.0%; Conservative

Score 519.2; DB 7; Pred. No. 6.1e-133; 0; Mismatches 8;

Length Indels

593;

ω •-

Gaps

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REFERENCE
AUTHORS
TITLE
JOURNAL
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CD520319
LOCUS
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ORGANISM
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VERSION
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                 CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM200 row: k column: 07
High quality sequence stop: 563.
Location/Qualifiers
                                                                                                                                                                                        National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
                                                                                                                                                                                                                                                                      Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                         1 (bases 1 to 757)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CD520319.1 GI:31452037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD520319 757 bp mRNA linear ES' AGENCOURT 14360077 NIH MGC 191 Homo sapiens cDNA clone IMAGE:30410454 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATGTTGGATGAAGAAA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTATAATCCTTTTGGGAATTTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
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                                                       RESULT 41
CD723203
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                                       DEFINITION
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Best Local Similarity
Matches 539; Conserv
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CD723203 588 bp
oj19b07.y1 Human lacrimal gland,
clone oj19b07 5', mRNA sequence.
CD723203
                                                                                                                                                                                                                                                                                                                               CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
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                                                                                                                                                                                                                                                                                                           CACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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/tlissue_type="Pooled"
/tlissue_type="Pooled"
/lab_nost="PullOB (TI phage-resistant)"
/clone_lib="NIH_MGC_191"
/clone_lib="NIH_MGC_191"
/clone_lib="NIH_MGC_191"
/clone="Yvector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/inte="Yvector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/inte="Yvector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/inte = "Yvector: policy of the primed and directionally cloned for majorate site in clones and N = A, C, G, G, or T). Average insert site 1.69
/kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                          578
                                                                                                                                                      652
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/mol_type="mRNA"
/db_xref="taxon:9606"
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                   mRNA linear EST 26-JUN-200 unamplified: oj Homo sapiens cDNA
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EST 26-JUN-2003

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                                                                                                                                                                                                                                                                                                              211 GAAGATCAACAAGAACCTCAATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAA
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Plate: 19 row: b column: 07
Seq primer: M13RP1 reverse primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dickinson,D., Laurie,G. and Wistow,G. Expressed sequence tag analysis of human lacrimal Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 588)
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CAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGC
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                                                          CAGGCTGTTAAATGAATGCAGAGAGAGTGCTGCACCAAATCATTCAGCGCCACCTCACTGC
                                                                                          CAGGCTGTTAAATGAATGCAGAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGC
                                                                                                                                                                          TGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Human lacrimal gland, unamplified: oj"
/note="Organ: Eye; Vector: pCW/Sport6; RNA was extracted
from 2 human lacrimal glands. A directionally cloned cDNA
library in the pCM/SPORT6 vector(Life Technologies) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's Instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adapter
[5'.pGACTAGTTCTAGATCGCGAGCGGCCCCC((T)15-3']. EST analysis
was performed on the unamplified library at the NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Eye Institute
NIH, Bethesda, MD 20892-2740,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lacrimal gland"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="oj19b07"
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|mol_type="mRNA"
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                                                                                                                                                                              180 GGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                              510;
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                                                                                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                                                                                            س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jap
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizushima-Sugano,J., Nakai,K. and Sugano,S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
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Suzuki,Y., Yamashita,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP345938 Sugano cDNA library, synovial membrane Homo sapiens clone SYN08154, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG
                                                     TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG
                                                                                              TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
                                                                                                                                                                                                                             CCACCATCATAATAGACGACAAGTAGTGGGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                                                                                                               CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="synovial membrane"
/clone_lib="Sugano cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SYN08154"
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Pred. No. 5.3e-127;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469M0735
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (Dases 1 to 605)

Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemer, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR771295
CR771295.1 GI:52614568
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemai
Molecular Genome Analysis, German Cancer Research Center (DKRZ);
Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pongo pygmaeus mRNA (Poustka,A., 
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKFZp469M0735_r1 469 (synonym: DKFZp469M0735_5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pongo pygmaeus (orangutan)
Pongo pygmaeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiemann,S.
                                                                                     TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGAGAAGA
                                                                                                                                    TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
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                                                                                                                                                                    GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                        TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
                   TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                       /tissue_type="kidney"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: Sfila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pongo pygmaeus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                            DB 7;
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National Institutes of Health,
Unpublished (1999)
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603045171F1 NIH_MGC_116 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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Plate: LLAM11463 row: m column:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
                                                                                                                                                     /Clone lib="NIH MGC 116"
//Clone lib="NIH MG
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/db_xref="taxon:9606"
/clone="IMAGE:5185720"
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/mol_type="mRNA"
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                              82.3%;
97.5%;
Score 494.6; DB 4;
Pred. No. 4.4e-126;
0; Mismatches 9;
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library
Vector sequences were eliminated by RepeatMasker and crossmatch version 0.990319
                                                          Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried
Animal Genome Research Program (Japan) by National Institute
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped co
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 773)

Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H. Okumura,N., Hamasima,N. and Awata,T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP433798 full-length enriched swine cDNA linear EST 30-DEC-2003 scrofa cDNA clone LNG010079A10 5', mRNA sequence.

BP433798
                                                                                                                                                                            Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
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/dev_stage="adult"
/clone_lib="full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="LNG010079A10"
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91.5%;
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